GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 26, 2002, 08:04:11 ; Search time 23.85 Seconds
(without alignments)
15.529 Million cell updates/sec

Title: US-09-658-315-9
Perfect score: 26
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101:*
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2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	100.0	5	17	AAR95670	Angiotensin II fra
2	26	100.0	5	19	AAW64736	Angiotensin II pep
3	26	100.0	5	19	AAW65605	Angiotensin II ana
4	26	100.0	5	19	AAW71118	Peptide AII(1-5) u
5	26	100.0	5	20	AAY49594	Angiotensin analog
6	26	100.0	5	20	AAY33909	Angiotensin II ana
7	26	100.0	5	20	AAY30547	Amino acid sequenc
8	26	100.0	5	20	AAY30591	Amino acid sequenc
9	26	100.0	5	20	AAY32722	Angiotensin II ana
10	26	100.0	5	20	AAY33776	Angiotensin II (AI
11	26	100.0	5	20	AAY15353	Angiotensin II (AI
12	26	100.0	5	20	AAY15313	Angiotensin II (AI
13	26	100.0	5	21	AAB27409	Angiotensin II ana
14	26	100.0	5	21	AAB28107	Angiotensin II ana
15	26	100.0	5	21	AAY84568	Amino acid sequenc
16	26	100.0	5	21	AAY84132	Peptide comprising
17	26	100.0	5	21	AAY77045	Angiotensin II (AI
18	26	100.0	5	21	AAY57409	Angiotensin peptid
19	26	100.0	5	22	AAE02996	Human angiotensin
20	26	100.0	5	22	AAE03159	Human angiotensin
21	26	100.0	5	22	AAB60413	C-terminally trunc
22	26	100.0	6	17	AAR95669	Angiotensin II fra
23	26	100.0	6	19	AAW65604	Angiotensin II ana
24	26	100.0	6	19	AAW64735	Angiotensin II pep
25	26	100.0	6	19	AAW71117	Peptide AII(1-6) u
26	26	100.0	6	20	AAY49593	Angiotensin analog
27	26	100.0	6	20	AAY33908	Angiotensin II ana
28	26	100.0	6	20	AAY30546	Amino acid sequenc
29	26	100.0	6	20	AAY30590	Amino acid sequenc
30	26	100.0	6	20	AAY32721	Angiotensin II ana
31	26	100.0	6	20	AAY33775	Angiotensin II (AI
32	26	100.0	6	20	AAY15352	Angiotensin II (AI
33	26	100.0	6	20	AAY15312	Angiotensin II (AI
34	26	100.0	6	21	AAB27408	Angiotensin II ana
35	26	100.0	6	21	AAB28106	Angiotensin II ana
36	26	100.0	6	21	AAY84131	Peptide comprising
37	26	100.0	6	21	AAY77044	Angiotensin II (AI
38	26	100.0	6	21	AAY57408	Angiotensin peptid
39	26	100.0	6	22	AAE02995	Human angiotensin
40	26	100.0	6	22	AAE03158	Human angiotensin
41	26	100.0	7	17	AAR95665	Angiotensin II fra
42	26	100.0	7	19	AAW65600	Angiotensin II ana
43	26	100.0	7	19	AAW64731	Angiotensin II pep
44	26	100.0	7	19	AAW71113	Peptide AII(1-7) u
45	26	100.0	7	20	AAY49589	Angiotensin analog

ALIGNMENTS

RESULT 1
AAR95670
ID AAR95670 standard; peptide; 5 AA.
XX
AC AAR95670;
XX
DT 09-JAN-1997 (first entry)
XX
DE Angiotensin II fragment AII(1-5).
XX
KW Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;
KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;
KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.
XX
OS Synthetic.
XX
PN WO9614858-A1.
XX
PD 23-MAY-1996.
XX
PF 14-NOV-1995; 95WO-US14764.
XX
PR 06-JUN-1995; 95US-0465775.
PR 14-NOV-1994; 94US-0337781.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers K;
XX
DR WPI; 1996-259561/26.
XX
PT Accelerating wound healing by application of angiotensin II
PT fragments - are effective at very low concn. and do not cause
PT hypertension

XX
PS Disclosure; Page 4; 46pp; English.
XX
CC AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see
CC AAR95662) is an octapeptide present in humans and other species. AT2 is
CC one of the most potent vasoconstrictors known, causing constriction of
CC the arterioles. The formation of angiotensin is initiated by the action
CC of renin on angiotensinogen. The substance formed is a decapeptide
CC called angiotensin I which is converted by the enzyme angiotensinase (by
CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release
CC of extracellular matrices involved in wound repair. These fragments can
CC be used in a compound for accelerating wound healing. The compounds are
CC administered as matrical or micellar solutions, formulated with a
CC carrier or diluent, alternatively the compound is applied in conjuncture
CC with a wound dressing. The carrier used in the composition is
CC preferably carboxymethylcellulose, crystaloids, viscoelastics, or poly
CC glycols. By using fragments of this sequence (or analogues of it),
CC growth as well as healing of tissues is improved, such as in cases of
CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or
CC intraperitoneal surgical wounds. The compounds containing the AT2
CC fragments are less hypertensive than full length AT2, and are also
CC effective at much lower (nanomolar) concentrations than full length AT2.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 drvyi 5

RESULT 2
AAW64736
ID AAW64736 standard; peptide; 5 AA.
XX
AC AAW64736;
XX
DT 02-NOV-1998 (first entry)
XX
DE Angiotensin II peptide #8.
XX
KW Proliferation; mesenchymal stem cell; lineage-specific cell;
KW haematopoietic; cell culture; transplantation; treatment; malignant;
KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9832457-A2.
XX
PD 30-JUL-1998.
XX
PF 26-JAN-1998; 98WO-US01552.
XX
PR 23-JAN-1998; 98US-0066593.
PR 28-JAN-1997; 97US-0036507.
PR 08-MAY-1997; 97US-0046859.
PR 28-OCT-1997; 97US-0063684.
PR 31-OCT-1997; 97US-0063910.
PR 18-NOV-1997; 97US-0065612.
PR 26-NOV-1997; 97US-0066593.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI diZerega G, Rodgers KE;
XX
DR WPI; 1998-437044/37.
XX
PT Promoting haematopoietic and mesenchymal cell proliferation and
PT differentiation - by contacting the cells with angiotensinogen,
PT angiotensin I or II, or analogues or fragments of these
XX
PS Claim 7; Page 14; 114pp; English.
XX
CC AAW64728-W64763 are peptides used in a novel method for accelerating the
CC proliferation of mesenchymal stem cells (MSCs), haematopoietic
CC lineage-specific cells or mesenchymal lineage-specific cells. The method
CC involves contacting the cells with an active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R1-R8 in
CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together
CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,
CC Ala, Leu, norLeu, Ile, Gly, Pro, Aib, Acpc (1-aminocyclopentane
CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(PO3)2, Thr, Ser, homoSer or
CC azaTyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or
CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are
CC not defined in the specification, the peptide bond between Ra and Rb is
CC labile to aminopeptidase A cleavage excluding sequences including R4 as a
CC terminal Tyr group. A second active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R2-R8 in
CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,
CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is alos
CC described. The inventions are particularly useful in cell culture
CC mediums. These cells may be used in transplantation techniques for
CC treatment of malignant or inherited diseases. The formulae represent
CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),
CC or AII AT2 type 2 receptor agonists.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 drvyi 5

RESULT 3
AAW65605
ID AAW65605 standard; peptide; 5 AA.
XX
AC AAW65605;
XX
DT 09-NOV-1998 (first entry)
XX
DE Angiotensin II analogue, AII(1-5).
XX
KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;
KW wound healing.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9826795-A1.
XX
PD 25-JUN-1998.
XX
PF 16-DEC-1997; 97WO-US23461.
XX
PR 15-DEC-1997; 97US-0990664.
PR 16-DEC-1996; 96US-0028310.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers KE;
XX
DR WPI; 1998-362518/31.
XX
PT Promoting incorporation of skin graft onto underlying tissue -
PT comprises pre-treating graft with angiotensin II, or analogue or

PT peptide fragment
XX
PS Disclosure; Page 6; 82pp; English.
XX
CC The invention relates to the use of angiotensin II (AII), AII analogues,
CC AII fragments and AII fragment analogues for promoting incorporation of a
CC skin graft into underlying tissue of a mammal. The peptides are effective
CC in accelerating the growth or healing of skin grafts and in accelerating
CC re-epithelisation and tissue repair, even at very low concentrations.
CC They can significantly accelerate the rate of healing at nanomolar levels
CC in vivo. AII accelerates wound repair by increased neovascularisation,
CC growth factor release, re-epithelisation, extracellular matrix production
CC and increased flow of blood and nutrients to the injured tissue. Use of
CC the above peptides other than AII itself (an extremely potent vaso-
CC constrictor) may avoid the side-effects of AII, such as increase in blood
CC pressure and thirst. The present sequence represents an angiotensin
CC II fragment.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 drvyi 5

RESULT 4
AAW71118
ID AAW71118 standard; peptide; 5 AA.
XX
AC AAW71118;
XX
DT 27-OCT-1998 (first entry)
XX
DE Peptide AII(1-5) used to accelerate thermal wound healing.
XX
KW Angiotensin; AII; acceleration; thermal wound healing; human;
KW growth factor release; neovascularisation; re-epithelialisation;
KW extracellular matrix production.
XX
OS Synthetic.
XX
PN WO9833813-A2.
XX
PD 06-AUG-1998.
XX
PF 04-FEB-1998; 98WO-US02049.
XX
PR 04-FEB-1997; 97US-0037166.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI DiZerega G, Rodgers KE;
XX
DR WPI; 1998-437391/37.
XX
PT Methods for accelerating thermal wound healing in humans - using
PT angiotensinogen II and AII analogues
XX
PS Claim 3; Page 9; 58pp; English.
XX
CC AAW71110-27 represent peptide used in the method of the invention. The
CC specification describes a method of accelerating thermal wound healing
CC in humans. The method comprises applying to the thermally injured tissue
CC an amount of at least one active agent which comprises the peptides
CC AAW71115-27. The method can be used to promote the healing of thermal
CC wounds by accelerating growth factor release, neovascularisation,
CC re-epithelialisation and extracellular matrix production. The sequences
CC are analogues of the angiotensin or angiotensinogen family of proteins.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 drvyi 5

RESULT 5
AAY49594
ID AAY49594 standard; peptide; 5 AA.
XX
AC AAY49594;
XX
DT 13-JAN-2000 (first entry)
XX
DE Angiotensin analogue peptide SEQ ID NO:9.
XX
KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;
KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.
XX
OS Synthetic.
XX
PN WO9952540-A1.
XX
PD 21-OCT-1999.
XX
PF 07-APR-1999; 99WO-US07654.
XX
PR 09-APR-1998; 98US-0081262.
PR 12-JUN-1998; 98US-0089024.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-620285/53.
XX
PT Treating or preventing infections in mammals using peptides derived
PT from angiotensin or angiotensin receptor agonists -
XX
PS Claim 2; Page 10; 91pp; English.
XX
CC The present invention describes a method for treating or preventing
CC infections in mammals by administering peptides (A) that are fragments
CC or analogues (or their fragments) of angiotensinogen, angiotensins I or
CC II, or angiotensin II AT_2-type receptor agonists. (A) contain at least
CC 3 consecutive amino acids (aa) from the sequence (S1):
CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;
CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane
CC carboxylic acid), Ala, dimethylglycine, Pro, betaine, Glu(NH_2), Gly,
CC Asp(NH_2) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,
CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,
CC Ile, Gly, Pro, Aib (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr
CC (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;
CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;
CC R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =
CC sequences having R4 as a terminal Tyr residue are excluded. The method
CC is particularly used in cases of bacterial infection (e.g. septic shock,
CC peritonitis, bacteraemia or endotoxaemia) but also against viral and
CC parasitic infections. AAY49586 to AAY49623 represent specifically
CC claimed examples of (A).
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;

```
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 drvyi 5


RESULT   6
AAY33909
ID   AAY33909 standard; peptide; 5 AA.
XX
AC   AAY33909;
XX
DT   29-NOV-1999  (first entry)
XX
DE   Angiotensin II analogue AII(1-5).
XX
KW   embryonic stem cell; ES; angiotensin; totipotent cell;
KW   gene therapy; replacement therapy; angiotensin II; AII;
KW   analogue.
XX
OS   Homo sapiens.
XX
PN   WO9942122-A1.
XX
PD   26-AUG-1999.
XX
PF   16-FEB-1999;   99WO-US03243.
XX
PR   19-FEB-1998;   98US-0075179.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Dizerega G,  Rodgers KE;
XX
DR   WPI; 1999-527419/44.
XX
PT   Promoting embryonal cell proliferation, using angiotensinogen and
PT   angiotensin peptides, analogs or fragments
XX
PS   Claim 2; Page 8; 76pp; English.
XX
CC   This is the amino acid sequence of the Angiotensin II analogue,
CC   AII(1-5). The formation of Angiotensin II (AII) is initiated by the
CC   action of renin on the plasma substrate angiotensinogen.
CC   This results in Angiotensin I (AI) which then converted to AII by the
CC   converting enzyme angiotensinase which removes the C-terminal His-Leu
CC   residues from AI (AAY42372).
CC   Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and
CC   analogs, Angiotensin II (AII), AII analogs, AII fragments or analogs,
CC   or AII AT2 type 2 receptor agonists can rapidly provide a large
CC   population of ESCs (Embryonic Stem Cell) for use in replacement
CC   therapy. Similarly, methods that increase in vivo proliferation of
CC   ESCs will enhance the utility of replacement therapy by rapidly
CC   increasing local concentration of the stem cells and their progeny at
CC   the site of therapy.
CC   The method also increases the potential utility of ESCs as vehicles
CC   for gene therapy in certain disorders by more efficiently providing
CC   a large number of such cells for transfection, and also by providing a
CC   more efficient means to rapidly expand transfected ESCs.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 26;  DB 20;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 drvyi 5


RESULT   7
AAY30547
ID   AAY30547 standard; peptide; 5 AA.
XX
AC   AAY30547;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Amino acid sequence of angiotensin II fragment AII1-5.
XX
KW   Angiotensin; analogue; tissue equivalent; cell proliferation.
XX
OS   Synthetic.
XX
PN   WO9946285-A2.
XX
PD   16-SEP-1999.
XX
PF   11-MAR-1999;   99WO-US05261.
XX
PR   11-MAR-1998;   98US-0077499.
PR   12-JUN-1998;   98US-0089064.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers KE,  Dizerega G;
XX
DR   WPI; 1999-551360/46.
XX
PT   An improved method for producing a tissue equivalent with angiotensin I
PT   and II derived active agents  -
XX
PS   Claim 2; Page 56; 83pp; English.
XX
CC   AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII
CC   fragments and AII analogues. The peptides are used in the method
CC   of the invention. The specification describes an improved method
CC   for producing a tissue equivalent. The method comprises contacting
CC   the tissue equivalent with angiotensin I and II derived active
CC   agents. The methods are used for production and culture of tissue
CC   equivalents (three-dimensional cell and tissue culture systems),
CC   chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,
CC   vascular graft, cartilage, ligament, collagen lattice, liver and
CC   kidney tissue equivalents. The methods and tissue culture systems
CC   are used for the long-term proliferation of cells and tissues
CC   in an in vitro environment that more closely approximates that found
CC   in vivo.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 26;  DB 20;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 drvyi 5


RESULT   8
AAY30591
ID   AAY30591 standard; peptide; 5 AA.
XX
AC   AAY30591;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Amino acid sequence of an angiotensin II (AII) fragment AII1-5.
XX
KW   Angiotensin; analogue; radiation mitigation; tissue damage;
KW   radiation therapy; bone marrow transplantation;
KW   megakaryocyte production; platelet production; cancer therapy;
```

KW gene therapy; hematopoietic disorder.
XX
OS Synthetic.
XX
PN WO9945945-A1.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US05194.
XX
PR 10-MAR-1998; 98US-0077382.
PR 09-APR-1998; 98US-0081262.
PR 30-APR-1998; 98US-0083670.
PR 19-JUN-1998; 98US-0090096.
PR 22-JUN-1998; 98US-0090216.
PR 11-SEP-1998; 98US-0099957.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
PA (RODG/) RODGERS K E.
PA (DIZE/) DIZEREGA G.
XX
PI Rodgers KE, Dizerega G;
XX
DR WPI; 1999-551209/46.
XX
PT Use of angiotensin and angiotensin type peptides, for mitigating
PT radiation induced tissue damage, improving bone marrow transplantation
PT and promoting megakaryocyte and platelet production -
XX
PS Claim 2; Page 89; 116pp; English.
XX
CC AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII
CC fragments and AII analogues. The peptides are used in the method
CC of the invention. The specification describes a method for mitigating
CC radiation induced tissue damage, improving the effectiveness of
CC radiation therapy, to support bone marrow transplantation, and
CC promoting megakaryocyte production and mobilization and platelet
CC production. The method comprises administration of the present peptides.
CC The methods can be used to mitigate radiation induced tissue damage, to
CC improve the effectiveness of radiation therapy, to support bone marrow
CC transplantation, and to promote megakaryocyte production and
CC mobilization and platelet production. They are used particularly in
CC cancer therapy. They can also be used to provide megakaryocytes as
CC vehicles for gene therapy in hematopoietic disorders, by providing a
CC more efficient means to rapidly expand transfected megakaryocytes.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 drvyi 5

RESULT 9
AAY32722
ID AAY32722 standard; peptide; 5 AA.
XX
AC AAY32722;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II analogue AII(1-5).
XX
KW Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;
KW chemotaxis; growth factor; liver regeneration; cirrhosis;
KW hepatocarcinoma; hepatectomy; transplantation.
XX
OS Synthetic.
XX
PN WO9939743-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02618.
XX
PR 13-NOV-1998; 98US-0108412.
PR 09-FEB-1998; 98US-0074104.
XX
PA (DIZE/) DIZEREGA G.
PA (RODG/) RODGERS K E.
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508461/42.
XX
PT Hepatic cell proliferation with angiotensin I and II derived active
PT agents, useful for regeneration of liver after resection
XX
PS Claim 2; Page 9; 66pp; English.
XX
CC Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The
CC peptides are derived from the AII peptide (AAY32750). AII increases
CC mitogenesis and chemotaxis in cultured cells, and also increases the
CC release of growth factors and extracellular matrices. AII has also been
CC shown to increase the proliferation of certain cell types. The AII
CC analogue peptides can be used as the active agent in a method for
CC promoting hepatic cell proliferation and differentiation. The method
CC involves contacting the hepatic cells with an amount effective enough to
CC promote proliferation of any of the peptides. This method is useful in
CC liver regeneration following resection of hepatocarcinomas, hepatitis
CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic
CC failure, hepatocyte transplantation, liver transplantation and other
CC hepatic disorders where rapid regeneration of the liver is desirable. The
CC methods are also useful in rapidly providing a large population of
CC hepatic cells for use in cell therapy and for providing a large
CC population of transfected hepatic cells for use in gene therapy.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 drvyi 5

RESULT 10
AAY33776
ID AAY33776 standard; peptide; 5 AA.
XX
AC AAY33776;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) octapeptide fragment AII(1-5).
XX
KW Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;
KW neuronal cell proliferation; differentiation; Alzheimer's disease;
KW Parkinson's disease; neuron replacement therapy.
XX
OS Homo sapiens.
XX
PN WO9942123-A1.
XX
PD 26-AUG-1999.
XX

PF 19-FEB-1999; 99WO-US03772.
XX
PR 19-FEB-1998; 98US-0075232.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-527420/44.
XX
PT Promoting neuronal cell proliferation and differentiation
XX
PS Claim 2; Page 10; 62pp; English.
XX
CC Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin
CC II (AII) octapeptide (AAY33768) and they have AT2 agonist activity. The
CC application of angiotensin to wound tissue significantly increases the
CC rate of wound healing. AII is known to increase mitogenesis and
CC chemotaxis in cultured cells, and also increases their release of growth
CC factors and extracellular matrices, implicating it in cell growth and
CC differentiation. AT2 receptors are receptors for AII and are thought to
CC be involved in the mediation of the cell differentiation effects of AII.
CC Peptides AAY33768-Y33802 are used in a method for promoting neuronal
CC cell proliferation or differentiation. This method is useful in the
CC treatment of Alzheimer's and Parkinson's diseases by neuron replacement
CC therapy.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 drvyi 5

RESULT 11
AAY15353
ID AAY15353 standard; peptide; 5 AA.
XX
AC AAY15353;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) analogue, AII(1-5).
XX
KW burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;
KW AII; analogue; chronic renal failure; cancer; bone marrow.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9940106-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02648.
XX
PR 09-DEC-1998; 98US-0111535.
PR 09-FEB-1998; 98US-0074106.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508486/42.
XX
PT Promoting erythropoiesis with angiotensin I and II derived active
PT agents, useful for treatment of, e.g. congenital or acquired
PT aplastic or hypoplastic anemia
XX
PS Claim 2; Page 10; 76pp; English.
XX
CC This sequence is an angiotensin II (AII) analogue. Similar sequences
CC also based on the AII peptide have been tested against each other, AII
CC and a negative control. These active agents have been shown to affect
CC the levels of BFU-E (burst forming units-erythroid) in culture.
CC The active agents (AAY15348, AAY15359, AAY15372, AAY15379, and AAY15380)
CC augment erythropoiesis by potentiating erythropoietin-induced
CC differentiation. Increasing the rate of erythropoiesis improves clinical
CC benefits for the treatment of congenital or acquired aplastic or
CC hypoplastic anemia associated with chronic renal failure, end-stage renal
CC disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy,
CC bone marrow transplantation and chronic diseases.
CC The active agents permit the use of smaller doses of erythropoietin
CC therefore decreasing treatment costs.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 drvyi 5

RESULT 12
AAY15313
ID AAY15313 standard; peptide; 5 AA.
XX
AC AAY15313;
XX
DT 09-NOV-1999 (first entry)
XX
DE Angiotensin II (AII) analogue, AII(1-5).
XX
KW angiotensin; angiotensin II; AII; wound healing; scarring;
KW tissue repair; agonist; analogue.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9940107-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US02725.
XX
PR 09-FEB-1998; 98US-0074105.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega G, Rodgers KE;
XX
DR WPI; 1999-508487/42.
XX
PT Epithelial stem cell and keratinocyte proliferation with angiotensin
PT I and II derived active agents, useful for treatment of skin wounds
XX
PS Claim 2; Page 10; 70pp; English.
XX
CC This is the amino acid sequence of an Angiotensin II analogue. This and
CC other similar analogues (AAY15306 to AAY15316 and AAY15321 to AAY15337)
CC can be used to promote the proliferation of epithelial stem cells and
CC Keratinocytes leading to a more rapid and efficient cellular response to
CC stratified epithelial injury. The angiotensin analogues are derived from
CC an octapeptide present in humans and other species which has the
CC sequence of Asp-Arg-Val-Tyr-Ile-His-Pro-Phe (AAY15342) and is known as
CC angiotensin II (AII). This is formed by the action of renin on the
CC plasma substrate angiotensinogen, the product of this reaction is a

```
CC   decapeptide called angiotensin I (AI) which is converted to AII by the
CC   converting enzyme angiotensinase which removes the C-terminal His-Leu
CC   residues from AI (AAY15339).
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 26;  DB 20;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 drvyi 5


RESULT  13
AAB27409
ID   AAB27409 standard; Peptide; 5 AA.
XX
AC   AAB27409;
XX
DT   23-JAN-2001  (first entry)
XX
DE   Angiotensin II analog AII(1-5).
XX
KW   Angiotensinogen; AII; AII; myocyte proliferation; myocardial injury;
KW   cardiomyopathies; inflammation; infection; sepsis; ischemia;
KW   heart valve disease; myocarditis; angiotensin.
XX
OS   Synthetic.
XX
PN   WO200053211-A2.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000; 2000WO-US06198.
XX
PR   09-MAR-1999;   99US-0123678.
PR   31-AUG-1999;   99US-0151874.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers K,  Dizerega G;
XX
DR   WPI; 2000-611400/58.
XX
PT   Promoting myocyte proliferation and myocardial tissue repair by
PT   contacting myocytes with angiotensinogen or angiotensin I or II, useful
PT   for treating heart attacks, cardiomyopathies, inflammation and
PT   infection -
XX
PS   Claim 2; Page 10; 55pp; English.
XX
CC   The present invention relates to a method of promoting myocyte
CC   proliferation or differentiation by contacting myocytes with an active
CC   agent containing angiotensinogen, angiotensin I and II  (AI, AII), and
CC   angiotensin analogs. The present sequence is an angiotensin II analog
CC   of the invention. The active agents of the invention may be useful for
CC   promoting myocardial tissue repair following myocardial injury and for
CC   treating heart failure in a mammal. Administration to accelerate in
CC   vivo myocyte proliferation and/or to treat myocardial injuries can be
CC   used to treat cardiomyopathies, inflammation, infection, sepsis,
CC   ischemia, heart valve disease, myocarditis, inflammation, myocardial
CC   ischemia and infarction and for improving cardiac output by increasing
CC   stroke volume.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 26;  DB 21;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 drvyi 5


RESULT  14
AAB28107
ID   AAB28107 standard; Peptide; 5 AA.
XX
AC   AAB28107;
XX
DT   26-JAN-2001  (first entry)
XX
DE   Angiotensin II analogue SEQ ID NO: 9.
XX
KW   Wound; scar formation; healing; adhesion formation; AII;
KW   angiotensin II analogue; scar treatment.
XX
OS   Synthetic.
XX
PN   WO200056345-A2.
XX
PD   28-SEP-2000.
XX
PF   22-MAR-2000; 2000WO-US07669.
XX
PR   23-MAR-1999;   99US-0125707.
PR   16-JUN-1999;   99US-0139541.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Rodgers K,  Dizerega G;
XX
DR   WPI; 2000-587607/55.
XX
PT   Limiting scar or adhesion formation comprises administering at least
PT   one active agent comprising a peptide -
XX
PS   Claim 2; Page 10; 54pp; English.
XX
CC   The present invention is concerned with peptide analogues of angiotensin
CC   II (AII) which can be used to limit scar and adhesion formation. The
CC   application of AII to wound tissue results in a rapid increase in the
CC   rate of wound healing and causes the proliferation of certain cells, such
CC   as epithelial cells and keratinocytes. Analogues of the protein have been
CC   shown to reduce scar formation, and can be used not only to limit new
CC   scar formation but also to therapeutically treat existing scars. The
CC   wound types include lacerations, burns, punctures, trauma, ulcers,
CC   periodontal conditions, laparotomy and incisional wounds, revision of
CC   hypertrophic scars, genetic hypertrophic scars, keloid scars,
CC   contractures after burns and cosmetic surgical procedures.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 26;  DB 21;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 drvyi 5


RESULT  15
AAY84568
ID   AAY84568 standard; Peptide; 5 AA.
XX
AC   AAY84568;
XX
DT   25-JUL-2000  (first entry)
XX
```

DE Amino acid sequence of angiotensin I conversion product Ang(1-5).
XX
KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
KW chronic heart failure; acute heart failure; myocardial infarction;
KW renal failure.
XX
OS Homo sapiens.
XX
PN WO200018899-A2.
XX
PD 06-APR-2000.
XX
PF 29-SEP-1999; 99WO-US22976.
XX
PR 30-SEP-1998; 98US-0163648.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Acton LS, Robison KE, Hsieh FY;
XX
DR WPI; 2000-293140/25.
XX
PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
PT polypeptide useful for detecting an ACE-2 therapeutic for treating
PT hypertension, congestive heart failure, myocardial infarction,
PT atherosclerosis and renal failure -
XX
PS Disclosure; Fig 8; 138pp; English.
XX
CC AAY84563-68 represent angiotensin I conversion products. The
CC specification describes a human angiotensin converting enzyme-2 (ACE-2).
CC ACE-2 is expressed predominantly in kidneys and testis. The sequence of
CC the full length ACE-2 cDNA was determined from a clone obtained from a
CC cDNA library prepared from mRNA of a human heart of a subject who had
CC congestive heart failure. ACE-2 has significant sequence homologies with
CC ACE enzymes, and has also been shown to hydrolyse angiotensin I into
CC Ang.(1-9). The ACE-2 therapeutics are used to treat blood pressure
CC related diseases and conditions, such as hypertension, congestive heart
CC failure, chronic heart failure, acute heart failure, myocardial
CC infarction, atherosclerosis and renal failure.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYI 5
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Db      1 drvyi 5
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Job time: 748 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 26, 2002, 08:13:06 ; Search time 12.46 Seconds
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9.030 Million cell updates/sec

Title: US-09-658-315-9
Perfect score: 26
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	100.0	5	2	US-08-465-775-9	Sequence 9, Appli
2	26	100.0	5	3	US-09-208-337-9	Sequence 9, Appli
3	26	100.0	5	3	US-08-990-664-10	Sequence 10, Appl
4	26	100.0	5	4	US-09-373-962-9	Sequence 9, Appli
5	26	100.0	5	4	US-09-245-680-9	Sequence 9, Appli
6	26	100.0	5	4	US-09-198-806C-9	Sequence 9, Appli
7	26	100.0	5	4	US-09-352-191-9	Sequence 9, Appli
8	26	100.0	6	2	US-08-465-775-8	Sequence 8, Appli
9	26	100.0	6	3	US-09-208-337-8	Sequence 8, Appli
10	26	100.0	6	3	US-08-990-664-9	Sequence 9, Appli
11	26	100.0	6	4	US-09-373-962-8	Sequence 8, Appli
12	26	100.0	6	4	US-09-245-680-8	Sequence 8, Appli
13	26	100.0	6	4	US-09-198-806C-8	Sequence 8, Appli
14	26	100.0	6	4	US-09-352-191-8	Sequence 8, Appli
15	26	100.0	7	2	US-08-465-775-4	Sequence 4, Appli
16	26	100.0	7	3	US-09-208-337-4	Sequence 4, Appli
17	26	100.0	7	3	US-08-990-664-5	Sequence 5, Appli
18	26	100.0	7	4	US-09-373-962-4	Sequence 4, Appli
19	26	100.0	7	4	US-09-245-680-4	Sequence 4, Appli
20	26	100.0	7	4	US-09-198-806C-4	Sequence 4, Appli
21	26	100.0	7	4	US-09-352-191-4	Sequence 4, Appli
22	26	100.0	7	6	5451571-4	Patent No. 5451571
23	26	100.0	8	1	US-07-858-842-2	Sequence 2, Appli
24	26	100.0	8	1	US-08-021-839A-3	Sequence 3, Appli
25	26	100.0	8	1	US-08-184-935-2	Sequence 2, Appli
26	26	100.0	8	1	US-08-212-433A-29	Sequence 29, Appl
27	26	100.0	8	1	US-08-185-448-8	Sequence 8, Appli
28	26	100.0	8	1	US-07-776-272-1	Sequence 1, Appli
29	26	100.0	8	1	US-08-428-488-21	Sequence 21, Appl
30	26	100.0	8	1	US-08-337-781-1	Sequence 1, Appli
31	26	100.0	8	1	US-08-240-711-20	Sequence 20, Appl
32	26	100.0	8	1	US-08-594-117-1	Sequence 1, Appli
33	26	100.0	8	1	US-08-520-770-2	Sequence 2, Appli
34	26	100.0	8	1	US-08-457-753-20	Sequence 20, Appl
35	26	100.0	8	2	US-08-115-968-1	Sequence 1, Appli
36	26	100.0	8	2	US-08-115-968-3	Sequence 3, Appli
37	26	100.0	8	2	US-08-115-968-4	Sequence 4, Appli
38	26	100.0	8	2	US-08-465-774-1	Sequence 1, Appli
39	26	100.0	8	2	US-08-465-774-2	Sequence 2, Appli
40	26	100.0	8	2	US-08-360-784B-2	Sequence 2, Appli
41	26	100.0	8	2	US-08-623-833B-4	Sequence 4, Appli
42	26	100.0	8	2	US-08-465-775-1	Sequence 1, Appli
43	26	100.0	8	2	US-08-542-927-3	Sequence 3, Appli
44	26	100.0	8	3	US-08-716-256-29	Sequence 29, Appl
45	26	100.0	8	4	US-09-300-434-1	Sequence 1, Appli

ALIGNMENTS

```
RESULT   1
US-08-465-775-9
; Sequence 9, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-9


  Query Match             100.0%;  Score 26;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db       1 DRVYI 5
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```
RESULT   2
US-09-208-337-9
; Sequence 9, Application US/09208337
; Patent No. 6096709
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  Gere, diZerega
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS
;    TITLE OF INVENTION:  AND ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/208,337
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/465,775
;      FILING DATE:  06-JUN-1995
;      APPLICATION NUMBER:  08/337,781
;      FILING DATE:  14-NOV-1994
;      APPLICATION NUMBER:  08/126,368
;      FILING DATE:  24-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC010.001CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  949-760-0404
;      TELEFAX:  949-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Peptide
US-09-208-337-9


  Query Match             100.0%;  Score 26;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT   3
US-08-990-664-10
; Sequence 10, Application US/08990664
; Patent No. 6110895
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  diZerega, Gere
;    TITLE OF INVENTION:  METHOD OF PROMOTING HEALING
;    TITLE OF INVENTION:  IN SKIN GRAFTS
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/990,664
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,310
;      FILING DATE:  16-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-990-664-10


  Query Match             100.0%;  Score 26;  DB 3;  Length 5;
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  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT   4
US-09-373-962-9
; Sequence 9, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
;  FILE REFERENCE: 98364A
;  CURRENT APPLICATION NUMBER: US/09/373,962
;  CURRENT FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-5)
US-09-373-962-9


  Query Match             100.0%;  Score 26;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5
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RESULT   5
US-09-245-680-9
; Sequence 9, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method of Promoting Erythropoiesis
;  FILE REFERENCE: 98009B
;  CURRENT APPLICATION NUMBER: US/09/245,680B
;  CURRENT FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-5)
US-09-245-680-9


  Query Match             100.0%;  Score 26;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT   6
US-09-198-806C-9
; Sequence 9, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
;  APPLICANT:  Rodgers, Kathleen
;. APPLICANT:  diZerega, Gere
;  TITLE OF INVENTION:  Method for Promoting Mesenchymal Stem
;  TITLE OF INVENTION:  and Lineage-Specific Cell Proliferation
;  FILE REFERENCE:  97,017-F1
;  CURRENT APPLICATION NUMBER: US/09/198,806C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-5)
US-09-198-806C-9


  Query Match             100.0%;  Score 26;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT   7
US-09-352-191-9
; Sequence 9, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
;  TITLE OF INVENTION: Growth and Repair
;  FILE REFERENCE: 98365B
;  CURRENT APPLICATION NUMBER: US/09/352,191
;  CURRENT FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-5)
US-09-352-191-9


  Query Match             100.0%;  Score 26;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT   8
US-08-465-775-8
; Sequence 8, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-8


  Query Match             100.0%;  Score 26;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5
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```
RESULT   9
US-09-208-337-8
; Sequence 8, Application US/09208337
; Patent No. 6096709
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  Gere, diZerega
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS
;    TITLE OF INVENTION:  AND ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/208,337
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/465,775
;      FILING DATE:  06-JUN-1995
;      APPLICATION NUMBER:  08/337,781
;      FILING DATE:  14-NOV-1994
;      APPLICATION NUMBER:  08/126,368
;      FILING DATE:  24-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC010.001CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  949-760-0404
;      TELEFAX:  949-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Peptide
US-09-208-337-8


  Query Match             100.0%;  Score 26;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db       1 DRVYI 5


RESULT  10
US-08-990-664-9
; Sequence 9, Application US/08990664
; Patent No. 6110895
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen
;    APPLICANT:  diZerega, Gere
;    TITLE OF INVENTION:  METHOD OF PROMOTING HEALING
;    TITLE OF INVENTION:  IN SKIN GRAFTS
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/990,664
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,310
;      FILING DATE:  16-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  USC012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-990-664-9


  Query Match             100.0%;  Score 26;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db       1 DRVYI 5


RESULT  11
US-09-373-962-8
; Sequence 8, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
;  FILE REFERENCE: 98364A
;  CURRENT APPLICATION NUMBER: US/09/373,962
;  CURRENT FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-6)
US-09-373-962-8


  Query Match             100.0%;  Score 26;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
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Db      1 DRVYI 5


RESULT  12
US-09-245-680-8
; Sequence 8, Application US/09245680B
; Patent No. 6239109
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Method of Promoting Erythropoiesis
;  FILE REFERENCE: 98009B
;  CURRENT APPLICATION NUMBER: US/09/245,680B
;  CURRENT FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-6)
US-09-245-680-8


  Query Match             100.0%;  Score 26;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT  13
US-09-198-806C-8
; Sequence 8, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
;  APPLICANT:  Rodgers, Kathleen
;  APPLICANT:  diZerega, Gere
;  TITLE OF INVENTION:  Method for Promoting Mesenchymal Stem
;  TITLE OF INVENTION:  and Lineage-Specific Cell Proliferation
;  FILE REFERENCE:  97,017-F1
;  CURRENT APPLICATION NUMBER: US/09/198,806C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-6)
US-09-198-806C-8


  Query Match             100.0%;  Score 26;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT  14
US-09-352-191-8
; Sequence 8, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
;  APPLICANT: Rodgers, Kathleen
;  APPLICANT: diZerega, Gere
;  TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
;  TITLE OF INVENTION: Growth and Repair
;  FILE REFERENCE: 98365B
;  CURRENT APPLICATION NUMBER: US/09/352,191
;  CURRENT FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AII (1-6)
US-09-352-191-8


  Query Match             100.0%;  Score 26;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT  15
US-08-465-775-4
; Sequence 4, Application US/08465775
; Patent No. 5955430
;  GENERAL INFORMATION:
;    APPLICANT:  Rodgers, Kathleen E.
;    APPLICANT:  diZerega, Gere S.
;    TITLE OF INVENTION:  USE OF ANGIOTENSIN II FRAGMENTS AND
;    TITLE OF INVENTION:  ANALOGS THEREOF IN TISSUE REPAIR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o Robbins, Berliner & Carson
;      STREET:  201 No. 5955430th Figueroa Street #500
;      CITY:, Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,775
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spitals, John P.
;      REGISTRATION NUMBER:  29,215
;      REFERENCE/DOCKET NUMBER:  1920-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 977-1001
;      TELEFAX:  (213) 977-1003
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-465-775-4


  Query Match             100.0%;  Score 26;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
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Db 1 DRVYI 5

Search completed: February 26, 2002, 08:16:58
Job time: 232 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 26, 2002, 08:14:01 ; Search time 12.81 Seconds
(without alignments)
29.732 Million cell updates/sec

Title: US-09-658-315-9
Perfect score: 26
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	100.0	10	2	S65432	angiotensin I - ho
2	26	100.0	14	2	A01250	angiotensin precur
3	26	100.0	15	2	A60834	angiotensin I prec
4	26	100.0	115	2	A48793	glycosylation-inhi
5	26	100.0	115	2	I52370	macrophage migrati
6	26	100.0	115	2	A44499	macrophage migrati
7	26	100.0	115	2	C47274	migration inhibito
8	26	100.0	167	2	F83686	hypothetical prote
9	26	100.0	195	1	B69441	conserved hypothet
10	26	100.0	238	2	E70337	ABC transporter -
11	26	100.0	248	2	T44932	3-oxoacyl-[acyl-ca
12	26	100.0	312	2	T00992	hypothetical prote
13	26	100.0	409	1	G69000	molybdenum cofacto
14	26	100.0	476	1	JC2318	angiotensin precur
15	26	100.0	477	1	ANRT	angiotensin precur
16	26	100.0	477	1	A29978	angiotensin precur
17	26	100.0	485	1	ANHU	angiotensin precur
18	26	100.0	509	2	T06300	hypothetical prote
19	26	100.0	518	2	B64449	2-isopropylmalate
20	26	100.0	540	2	S72233	transcription fact
21	26	100.0	575	1	HNNZSZ	hemagglutinin-neur
22	26	100.0	575	1	HNNZSH	hemagglutinin-neur
23	26	100.0	575	2	S12135	hemagglutinin-neur
24	26	100.0	576	1	HNNZS	hemagglutinin-neur
25	26	100.0	581	1	A37913	serine/threonine-s
26	26	100.0	614	2	T43121	hypothetical prote
27	26	100.0	644	2	G64938	hypothetical prote
28	26	100.0	644	2	F82145	conserved hypothet
29	26	100.0	644	2	H85788	hypothetical prote
30	26	100.0	661	2	C83843	hypothetical prote
31	26	100.0	676	1	WMBEX6	UL6 protein - huma
32	26	100.0	688	2	A44306	polyphosphate kina
33	26	100.0	688	2	G85893	polyphosphate kina
34	26	100.0	739	2	I40715	malate synthase (E
35	26	100.0	749	2	S77175	sensory transducti
36	26	100.0	778	2	T44761	probable preprotei
37	26	100.0	808	2	F70720	probable transloca
38	26	100.0	838	2	T40203	conserved hypothet
39	26	100.0	1062	2	H83966	carbamoyl-phosphat
40	26	100.0	1071	2	F39845	carbamoyl-phosphat
41	26	100.0	1076	2	A69409	carbamoyl-phosphat
42	26	100.0	1238	2	A64596	hypothetical prote
43	26	100.0	1296	1	BTCLAB	bontoxilysin (EC 3
44	26	100.0	1296	2	I40645	botulinum neurotox
45	26	100.0	3194	2	D71917	toxin-like outer m

ALIGNMENTS

RESULT 1
S65432
angiotensin I - horn fly (fragment)
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65432
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willad
Eur. J. Biochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the di
A;Reference number: S65431; MUID:96215437
A;Accession: S65432
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <WIJ>
A;Note: the source is designated as Haematobia irritans exigua

Query Match 100.0%; Score 26; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5
```

RESULT 2
A01250
angiotensin precursor - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Mar-1998
C;Accession: A92775; A01250
R;Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A;Reference number: A92775
A;Accession: A92775
A;Molecule type: protein
A;Residues: 1-14 <SKE>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; hormone; vasoconstrictor
F;1-10/Product: angiotensin I #status experimental <AN1>
F;1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 26; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5
```

RESULT 3
A60834
angiotensin I precursor - dog (fragment)
N;Alternate names: angiotensinogen I
N;Contains: angiotensin I
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C;Accession: A60834
R;Oliver, J.A.
Hypertension 11, 21-27, 1988
A;Title: Purification and partial characterization of canine angiotensinogen.
A;Reference number: A60834; MUID:88113996
A;Accession: A60834
A;Molecule type: protein
A;Residues: 1-15 <OLI>
C;Superfamily: antithrombin III
C;Keywords: glycoprotein; plasma
F;1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 26; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
||||| |
Db 1 DRVYI 5

RESULT 4
A48793
glycosylation-inhibiting factor - human
N;Alternate names: macrophage migration inhibitory 12.7K protein; sarcolectin
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jul-2000
C;Accession: A48793; A49612; A33838; A47274; S34300; S33277
R;Mikayama, T.; Nakano, T.; Gomi, H.; Nakagawa, Y.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 10056-10060, 1993
A;Title: Molecular cloning and functional expression of a cDNA encoding glycosylation-in
A;Reference number: A48793; MUID:94052102
A;Accession: A48793
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <MIK>
A;Cross-references: GB:L10612; NID:g402701; PIDN:AAA35892.1; PID:g402702
R;Paralkar, V.; Wistow, G.
Genomics 19, 48-51, 1994
A;Title: Cloning the human gene for macrophage migration inhibitory factor (MIF).
A;Reference number: A49612; MUID:94245178
A;Accession: A49612
A;Molecule type: DNA
A;Residues: 1-115 <PAR>
A;Cross-references: GB:L19686; NID:g307284; PIDN:AAA21814.1; PID:g307285
R;Weiser, W.Y.; Temple, P.A.; Witek-Giannotti, J.S.; Remold, H.G.; Clark, S.C.; David, J
Proc. Natl. Acad. Sci. U.S.A. 86, 7522-7526, 1989
A;Title: Molecular cloning of a cDNA encoding a human macrophage migration inhibitory fa
A;Reference number: A33838; MUID:90017510
A;Accession: A33838
A;Molecule type: mRNA
A;Residues: 1-105,'S',107-115 <WEI>
A;Cross-references: GB:M25639; NID:g188555; PIDN:AAA36315.1; PID:g188556
A;Experimental source: activated T cells
R;Wistow, G.J.; Shaughnessy, M.P.; Lee, D.C.; Hodin, J.; Zelenka, P.S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1272-1275, 1993
A;Title: A macrophage migration inhibitory factor is expressed in the differentiating ce
A;Reference number: A47274; MUID:93165679
A;Accession: A47274
A;Molecule type: mRNA
A;Residues: 10-115 <WIS>
A;Cross-references: GB:M95775; NID:g187180; PIDN:AAA36179.1; PID:g187181
A;Experimental source: fetal lens
A;Note: sequence extracted from NCBI backbone (NCBIN:124868, NCBIP:124871)
R;Bucala, R.; Mitchell, R.A.; Bernhagen, J.
submitted to the EMBL Data Library, June 1993
A;Reference number: S34300
A;Accession: S34300
A;Molecule type: mRNA
A;Residues: 1-115 <BUC>
A;Cross-references: EMBL:Z23063; NID:g312333; PIDN:CAA80598.1; PID:g312334
R;Zeng, F.Y.; Weiser, W.Y.; Kratzin, H.; Stahl, B.; Karas, M.; Gabius, H.J.
Arch. Biochem. Biophys. 303, 74-80, 1993
A;Title: The major binding protein of the interferon antagonist sarcolectin in humar
A;Reference number: S33277; MUID:93256574
A;Accession: S33277
A;Molecule type: protein
A;Residues: 3-24 <ZEN>
A;Experimental source: placenta
A;Note: there is no signal sequence; the mature protein starts with residue 3
C;Genetics:
A;Gene: GDB:MIF
A;Cross-references: GDB:138402; OMIM:153620
A;Map position: 22q11.2-22q11.2
A;Introns: 36/3; 94/2
A;Note: appears to be a single copy gene (see reference A49612)
C;Superfamily: bovine glycosylation-inhibiting factor
F;3-115/Product: macrophage migration inhibitory factor #status predicted <MAT>

Query Match 100.0%; Score 26; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
||||| |
Db 93 DRVYI 97

RESULT 5
I52370
macrophage migration inhibitory factor MIF [similarity] - rat
C;Species: Rattus sp. (rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I52370
R;Sakai, M.; Nishihira, J.; Hibiya, Y.; Koyama, Y.; Nishi, S.
Biochem. Mol. Biol. Int. 33, 439-446, 1994
A;Title: Glutathione binding rat liver 13k protein is the homologue of the macroph
A;Reference number: I52370; MUID:95038523
A;Accession: I52370
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <RES>
A;Cross-references: GB:S73424; NID:g663139; PIDN:AAB32392.1; PID:g663140
C;Superfamily: bovine glycosylation-inhibiting factor

Query Match 100.0%; Score 26; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
||||| |
Db 93 DRVYI 97

RESULT 6
A44499
macrophage migration inhibitory factor DER6 - mouse
N;Alternate names: glycosylation-inhibiting factor; migration inhibitory factor, 10k
C;Species: Mus musculus (house mouse)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A44499; S34299; B47274; I49691; S38325; I56259
R;Lanahan, A.; Williams, J.B.; Sanders, L.K.; Nathans, D.
Mol. Cell. Biol. 12, 3919-3929, 1992
A;Title: Growth factor-induced delayed early response genes.
A;Reference number: A44499; MUID:92375060

A;Accession: A44499
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-115 <LAN>
A;Experimental source: BALB/c 3T3 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:111643)
R;Bernhagen, J.; Calandra, T.; Mitchell, R.A.; Martin, S.; Tracey, K.J.; Manogue, K.; Vo
submitted to the EMBL Data Library, June 1993
A;Reference number: S34299
A;Accession: S34299
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <BER>
A;Cross-references: EMBL:Z23048; NID:g312220; PIDN:CAA80583.1; PID:g312221
R;Wistow, G.J.; Shaughnessy, M.P.; Lee, D.C.; Hodin, J.; Zelenka, P.S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1272-1275, 1993
A;Title: A macrophage migration inhibitory factor is expressed in the differentiating ce
A;Reference number: A47274; MUID:93165679
A;Accession: B47274
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 6-115 <WIS>
A;Cross-references: GB:L07607; NID:g191490; PIDN:AAA37111.1; PID:g191491
A;Experimental source: lens
A;Note: sequence extracted from NCBI backbone (NCBIN:124869, NCBIP:124872)
R;Mikayama, T.; Nakano, T.; Gomi, H.; Nakagawa, Y.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 10056-10060, 1993
A;Title: Molecular cloning and functional expression of a cDNA encoding glycosylation-in
A;Reference number: A48793; MUID:94052102
A;Accession: I49691
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <RES>
A;Cross-references: GB:L10613; NID:g402716; PIDN:AAA37693.1; PID:g402717
R;Bernhagen, J.; Calandra, T.; Mitchell, R.A.; Martin, S.B.; Tracey, K.J.; Voelter, W.;
Nature 365, 756-759, 1993
A;Title: MIF is a pituitary-derived cytokine that potentiates lethal endotoxaemia.
A;Reference number: S38325; MUID:94019845
A;Accession: S38325
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 2-28 <BE2>
A;Cross-references: EMBL:Z23048
R;Mitchell, R.; Bacher, M.; Bernhagen, J.; Pushkarskaya, T.; Seldin, M.F.; Bucala, R.
J. Immunol. 154, 3863-3870, 1995
A;Title: Cloning and characterization of the gene for mouse macrophage migration inhibit
A;Reference number: I56259; MUID:95221891
A;Accession: I56259
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-115 <RE2>
A;Cross-references: GB:L39357; NID:g790847; PIDN:AAA74321.1; PID:g790848
C;Genetics:
A;Gene: Mif
A;Introns: 36/3; 94/2
C;Superfamily: bovine glycosylation-inhibiting factor

Query Match 100.0%; Score 26; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 93 DRVYI 97

RESULT 7
C47274
migration inhibitory factor, 10K - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: C47274
R;Wistow, G.J.; Shaughnessy, M.P.; Lee, D.C.; Hodin, J.; Zelenka, P.S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1272-1275, 1993
A;Title: A macrophage migration inhibitory factor is expressed in the differentiati
A;Reference number: A47274; MUID:93165679
A;Accession: C47274
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-115 <WIS>
A;Cross-references: GB:M95776; NID:g212257; PIDN:AAA48939.1; PID:g212258
A;Experimental source: embryo, lens
A;Note: sequence extracted from NCBI backbone (NCBIN:124870, NCBIP:124873)
C;Superfamily: bovine glycosylation-inhibiting factor

Query Match 100.0%; Score 26; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 93 DRVYI 97

RESULT 8
F83686
hypothetical protein BH0294 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C;Accession: F83686
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Reference number: A83650; MUID:20263314
A;Accession: F83686
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-167 <STO>
A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04013.1; GSPDB
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0294

Query Match 100.0%; Score 26; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 61 DRVYI 65

RESULT 9
B69441
conserved hypothetical protein AF1531 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: B69441
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; D
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness,
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Syke
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing ar
A;Reference number: A69250; MUID:98049343
A;Accession: B69441
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-195 <KLE>
A;Cross-references: GB:AE000997; GB:AE000782; NID:g2689320; PIDN:AAB89717.1; PID:g2
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0038

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  Query Match           100.0%;  Score 26;  DB 1;  Length 195;
  Best Local Similarity  100.0%;  Pred. No. 57;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db      68 DRVYI 72


RESULT  10
E70337
ABC transporter - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Feb-2001
C;Accession: E70337
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666
A;Accession: E70337
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-238 <AQF>
A;Cross-references: GB:AE000689; NID:g2983082; PIDN:AAC06695.1; PID:g2983089; GB:AE0006
A;Experimental source: strain VF5
C;Genetics:
A;Gene: abcT7
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;17-210/Domain: ATP-binding cassette homology <ABC>
F;34-41/Region: nucleotide-binding motif A (P-loop)


  Query Match           100.0%;  Score 26;  DB 2;  Length 238;
  Best Local Similarity  100.0%;  Pred. No. 69;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db     202 DRVYI 206


RESULT  11
T44932
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [imported] - Agrobacterium tum
C;Species: Agrobacterium tumefaciens
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T44932
R;Kim, K.S.; Farrand, S.K.
J. Bacteriol. 178, 3275-3284, 1996
A;Title: Ti plasmid-encoded genes responsible for catabolism of the crown gall opine man
by the plant tumor.
A;Reference number: Z22872; MUID:96236046
A;Accession: T44932
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-248 <KIM>
A;Cross-references: EMBL:U19620; NID:g797330; PIDN:AAB07783.1; PID:g797334
A;Experimental source: strain 15955
C;Genetics:
A;Gene: mocC
A;Genome: plasmid pTi15955
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: oxidoreductase


  Query Match           100.0%;  Score 26;  DB 2;  Length 248;
  Best Local Similarity  100.0%;  Pred. No. 72;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db     221 DRVYI 225


RESULT  12
T00992
hypothetical protein At2g26590 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T9J22.26
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C;Accession: T00992; D84662
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.;
submitted to the EMBL Data Library, April 1998
A;Description: Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence.
A;Reference number: Z14161
A;Accession: T00992
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-312 <ROU>
A;Cross-references: EMBL:AC002505; NID:g2739359; PID:g2739383
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: D84662
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-312 <STO>
A;Cross-references: GB:AE002093; NID:g2739383; PIDN:AAC14506.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g26590; T9J22.26
A;Map position: 2
A;Introns: 11/3; 42/3; 62/3; 100/3; 124/2; 169/2; 210/1; 241/3; 267/3; 286/1


  Query Match           100.0%;  Score 26;  DB 2;  Length 312;
  Best Local Similarity  100.0%;  Pred. No. 91;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db      81 DRVYI 85


RESULT  13
G69000
molybdenum cofactor biosynthesis protein MoeA - Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: G69000
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge,
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: f
A;Reference number: A69000; MUID:98037514
A;Accession: G69000
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-409 <MTH>
A;Cross-references: GB:AE000873; GB:AE000666; NID:g2622101; PIDN:AAB85499.1; PID:g26
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1003
A;Start codon: TTG
C;Superfamily: molybdenum cofactor biosynthesis protein moeA-2


  Query Match           100.0%;  Score 26;  DB 1;  Length 409;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYI 5
          |||||
Db    131 DRVYI 135
```

RESULT 14
JC2318
angiotensin precursor - sheep
N;Alternate names: angiotensinogen
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JC2318; A25406
R;Nagase, M.; Suzuki, F.; Fukamizu, A.; Takeda, N.; Takeuchi, K.; Murakami, K.; Nakamura
Biosci. Biotechnol. Biochem. 58, 1884-1885, 1994
A;Title: Sequencing and expression of sheep angiotensinogen cDNA.
A;Reference number: JC2318; MUID:95072318
A;Accession: JC2318
A;Molecule type: mRNA
A;Residues: 1-476 <NAG>
A;Cross-references: DDBJ:D17520; NID:g575593; PIDN:BAA04470.1; PID:g1197183
A;Experimental source: liver
A;Note: the authors translated the codon TTC for residue 465 as Leu
R;Fernley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.
Eur. J. Biochem. 154, 597-601, 1986
A;Title: Purification and characterization of ovine angiotensinogen.
A;Reference number: A25406; MUID:86136099
A;Accession: A25406
A;Molecule type: protein
A;Residues: 25-37,'X',39 <FER>
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;24-476/Product: angiotensinogen #status predicted <MPT>
F;25-34/Product: angiotensin #status predicted <MAT>
F;295,362/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 26; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYI 5
          |||||
Db     25 DRVYI 29
```

RESULT 15
ANRT
angiotensin precursor - rat
N;Contains: angiotensin I; angiotensin II; angiotensin III
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 18-Jun-1999
C;Accession: A93945; A90456; A01251
R;Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983
A;Title: Cloning and sequenc analysis of cDNA for rat angiotensinogen.
A;Reference number: A93945; MUID:83169849
A;Accession: A93945
A;Molecule type: mRNA
A;Residues: 1-477 <OHK>
A;Cross-references: GB:L00094; GB:J00704; NID:g202912; PIDN:AAA98779.1; PID:g202914
R;Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.
Biochemistry 20, 7010-7015, 1981
A;Title: Rat angiotensinogen and Des(antiotensinI)angiotensinogen: purification, charact
A;Reference number: A90456; MUID:82091819
A;Accession: A90456
A;Molecule type: protein
A;Residues: 25-41 <BOU>
C;Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted in
e I (angiotensin-converting enzyme), primarily in the lungs.
C;Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and ang
sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I
C;Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma
ung.
C;Superfamily: antithrombin III
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-477/Product: angiotensinogen #status predicted <MPT>
F;25-34/Product: angiotensin I #status experimental <PP1>
F;25-32/Product: angiotensin II #status experimental <PP2>
F;26-32/Product: angiotensin III #status experimental <PP3>
F;295,319/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 26; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DRVYI 5
          |||||
Db     25 DRVYI 29
```

Search completed: February 26, 2002, 08:17:18
Job time: 197 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 26, 2002, 08:16:16 ; Search time 10.14 Seconds
(without alignments)
18.079 Million cell updates/sec

Title: US-09-658-315-9
Perfect score: 26
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	100.0	8	1	ANG2_BOTJA	Q10582 bothrops ja
2	26	100.0	14	1	ANGT_HORSE	P01016 equus cabal
3	26	100.0	114	1	MIF_CHICK	Q02960 gallus gall
4	26	100.0	114	1	MIF_HUMAN	P14174 homo sapien
5	26	100.0	114	1	MIF_MOUSE	P34884 mus musculu
6	26	100.0	114	1	MIF_RAT	P30904 rattus norv
7	26	100.0	436	1	TBX6_HUMAN	O95947 homo sapien
8	26	100.0	476	1	ANGT_SHEEP	P20757 ovis aries
9	26	100.0	477	1	ANGT_MOUSE	P11859 mus musculu
10	26	100.0	477	1	ANGT_RAT	P01015 rattus norv
11	26	100.0	485	1	ANGT_HUMAN	P01019 homo sapien
12	26	100.0	518	1	YB95_METJA	Q58595 methanococc
13	26	100.0	540	1	TBX6_MOUSE	P70327 mus musculu
14	26	100.0	575	1	HEMA_SEND5	P27562 sendai viru
15	26	100.0	575	1	HEMA_SENDF	P19758 sendai viru
16	26	100.0	575	1	HEMA_SENDJ	P06863 sendai viru
17	26	100.0	575	1	HEMA_SENDZ	P04853 sendai viru
18	26	100.0	576	1	HEMA_SENDH	P03425 sendai viru
19	26	100.0	581	1	MIK1_SCHPO	P30290 schizosacch
20	26	100.0	644	1	YEAG_ECOLI	P77391 escherichia
21	26	100.0	676	1	UL06_HSV11	P10190 herpes simp
22	26	100.0	687	1	PPK_ECOLI	P28688 escherichia
23	26	100.0	687	1	PPK_SALTY	O86090 salmonella
24	26	100.0	738	1	MASZ_CORGL	P42450 corynebacte
25	26	100.0	778	1	SEA2_MYCLE	O32922 mycobacteri
26	26	100.0	808	1	SEA2_MYCTU	Q50612 mycobacteri
27	26	100.0	1071	1	CARB_BACSU	P25994 bacillus su
28	26	100.0	1295	1	BXA_CLOBO	P10845 clostridium
29	25	96.2	10	1	ANG1_BOTJA	Q10581 bothrops ja
30	25	96.2	10	1	ANGT_BOVIN	P01017 bos taurus
31	25	96.2	10	1	ANGT_CHICK	P01018 gallus gall
32	25	96.2	114	1	MIF_BOVIN	P80177 bos taurus
33	25	96.2	114	1	MIF_MERUN	O55052 meriones un
34	25	96.2	178	1	BDH_BOVIN	Q02337 bos taurus
35	25	96.2	272	1	PK1_NPVAC	P41415 autographa
36	25	96.2	311	1	NFE2_RHIME	Q52994 rhizobium m
37	25	96.2	446	1	GGAA_BACSU	P46917 bacillus su
38	25	96.2	465	1	YC14_KLEPN	Q48460 klebsiella
39	25	96.2	488	1	GAL7_LACHE	Q00054 lactobacill
40	25	96.2	511	1	EGO_ECOLI	P77257 escherichia
41	25	96.2	539	1	PRIS_METJA	Q58175 methanococc
42	25	96.2	572	1	HEMA_PI3B	P06167 bovine para
43	25	96.2	574	1	CDAS_THEET	P29964 thermoanaer
44	25	96.2	583	1	SECD_TREPA	O83425 treponema p
45	25	96.2	588	1	YO6B_CAEEL	P34602 caenorhabdi

ALIGNMENTS

RESULT 1
ANG2_BOTJA
ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE ANGIOTENSIN-LIKE PEPTIDE II (FRAGMENT).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 100.0%; Score 26; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 DRVYI 5

RESULT 2
ANGT_HORSE
ID ANGT_HORSE STANDARD; PRT; 14 AA.
AC P01016;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANGIOTENSINOGEN [CONTAINS: ANGIOTENSIN I; ANGIOTENSIN II] (FRAGMENT).
GN SERPINA8 OR AGT.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
RT "The preparation, purification, and amino acid sequence of a
RT polypeptide renin substrate.";

```
RL   J. Exp. Med. 106:439-453(1957).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR   PIR; A01250; A01250.
DR   InterPro; IPR000215; Serpin.
DR   PROSITE; PS00284; SERPIN; PARTIAL.
KW   Vasoconstrictor; Plasma; Serpin.
FT   PEPTIDE       1     10       ANGIOTENSIN I.
FT   PEPTIDE       1      8       ANGIOTENSIN II.
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1759 MW;  2E9921F8EEEFBDD7 CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db      1 DRVYI 5


RESULT   3
MIF_CHICK
ID   MIF_CHICK      STANDARD;      PRT;   114 AA.
AC   Q02960;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   MACROPHAGE MIGRATION INHIBITORY FACTOR (MIF) (PHENYLPYRUVATE
DE   TAUTOMERASE).
GN   MIF.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lens;
RX   MEDLINE=93165679; PubMed=7679497;
RA   Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;
RT   "A macrophage migration inhibitory factor is expressed in the
RT   differentiating cells of the eye lens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).
CC   -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC       ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC       HOST DEFENSE. ALSO ACTS AS A PHENYLPYRUVATE TAUTOMERASE.
CC   -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M95776; AAA48939.1; -.
DR   PIR; C47274; C47274.
DR   HSSP; P14174; 1GIF.
DR   InterPro; IPR001398; MIF.
DR   Pfam; PF01187; MIF; 1.
DR   PROSITE; PS01158; MIF; 1.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine.
FT   ACT_SITE      1      1       CATALYTIC BASE (BY SIMILARITY).
FT   INIT_MET      0      0       BY SIMILARITY.
SQ   SEQUENCE   114 AA;  12353 MW;  A55222D00E6D05CF CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     92 DRVYI 96


RESULT   4
MIF_HUMAN
ID   MIF_HUMAN      STANDARD;      PRT;   114 AA.
AC   P14174;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   MACROPHAGE MIGRATION INHIBITORY FACTOR (MIF) (PHENYLPYRUVATE
DE   TAUTOMERASE) (GLYCOSYLATION-INHIBITING FACTOR) (GIF).
GN   MIF OR MMIF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90017510; PubMed=2552447;
RA   Weiser W.Y., Temple P.A., Witek-Giannotti J.S., Remold H.G.,
RA   Clark S.C., David J.R.;
RT   "Molecular cloning of a cDNA encoding a human macrophage migration
RT   inhibitory factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:7522-7526(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94245178; PubMed=8188240;
RA   Paralkar V., Wistow G.J.;
RT   "Cloning the human gene for macrophage migration inhibitory factor
RT   (MIF).";
RL   Genomics 19:48-51(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94052102; PubMed=8234256;
RA   Mikayama T., Nakano T., Gomi H., Nakagawa Y., Liu Y.C.,
RA   Iwamatsu A., Weiser W.Y., Ishizaka K., Sato M., Ishii Y.;
RT   "Molecular cloning and functional expression of a cDNA encoding
RT   glycosylation-inhibiting factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:10056-10060(1993).
RN   [4]
RP   SEQUENCE OF 9-114 FROM N.A.
RC   TISSUE=Lens;
RX   MEDLINE=93165679; PubMed=7679497;
RA   Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;
RT   "A macrophage migration inhibitory factor is expressed in the
RT   differentiating cells of the eye lens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).
RN   [5]
RP   SEQUENCE OF 1-10.
RC   TISSUE=Liver;
RX   MEDLINE=93162045; PubMed=1286669;
RA   Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA   Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA   Appel R.D., Hughes G.J.;
RT   "Human liver protein map: a reference database established by
RT   microsequencing and gel comparison.";
RL   Electrophoresis 13:992-1001(1992).
RN   [6]
RP   SEQUENCE OF 2-23.
RX   MEDLINE=93256574; PubMed=7683862;
RA   Zeng F.Y., Weiser W.Y., Kratzin H., Stahl B., Karas M., Gabius H.J.;
RT   "The major binding protein of the interferon antagonist sarcolectin
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RT   in human placenta is a macrophage migration inhibitory factor.";
RL   Arch. Biochem. Biophys. 303:74-80(1993).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX   MEDLINE=96338096; PubMed=8766818;
RA   Sugimoto H., Suzuki M., Nakagawa A., Tanaka I., Nishihira J.;
RT   "Crystal structure of macrophage migration inhibitory factor from
RT   human lymphocyte at 2.1-A resolution.";
RL   FEBS Lett. 389:145-148(1996).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=96181524; PubMed=8610159;
RA   Kato Y., Muto T., Tomura T., Tsumura H., Watarai H., Mikayama T.,
RA   Ishizaka K., Kuroki R.;
RT   "The crystal structure of human glycosylation-inhibiting factor is a
RT   trimeric barrel with three 6-stranded beta-sheets.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:3007-3010(1996).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX   MEDLINE=96224258; PubMed=8643551;
RA   Sun H.W., Bernhagen J., Bucala R., Lolis E.;
RT   "Crystal structure at 2.6-A resolution of human macrophage migration
RT   inhibitory factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:5191-5196(1996).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=99282199; PubMed=10353846;
RA   Lubetsky J.B., Swope M., Dealwis C., Blake P., Lolis E.;
RT   "Pro-1 of macrophage migration inhibitory factor functions as a
RT   catalytic base in the phenylpyruvate tautomerase activity.";
RL   Biochemistry 38:7346-7354(1999).
CC   -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC       ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC       HOST DEFENSE. ALSO ACTS AS A PHENYLPYRUVATE TAUTOMERASE.
CC   -!- SUBUNIT: HOMOTRIMER.
CC   -!- DISEASE: MIF ACTIVITY HAS BEEN DETECTED IN LEUKOCYTE CULTURE
CC       SUPERNATANTS OF MICE DURING ALLOGRAFT REJECTION, IN THE SYNOVIA
CC       OF PATIENTS WITH RHEUMATOID POLYARTHRITIS, AND IN A VARIETY OF
CC       CHRONIC INFLAMMATORY LOCI.
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z23063; CAA80598.1; -.
DR   EMBL; M25639; AAA36315.1; -.
DR   EMBL; M95775; AAA36179.1; -.
DR   EMBL; L10612; AAA35892.1; -.
DR   EMBL; L19686; AAA21814.1; -.
DR   PIR; A33838; A33838.
DR   PIR; S33277; S33277.
DR   PDB; 1GIF; 12-MAR-97.
DR   PDB; 1MIF; 07-DEC-96.
DR   PDB; 1P1G; 07-JUN-99.
DR   PDB; 1CGQ; 07-JUN-99.
DR   PDB; 1CA7; 30-JUN-99.
DR   SWISS-2DPAGE; P14174; HUMAN.
DR   MIM; 153620; -.
DR   InterPro; IPR001398; MIF.
DR   Pfam; PF01187; MIF; 1.
DR   PROSITE; PS01158; MIF; 1.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.
FT   INIT_MET      0      0
FT   ACT_SITE      1      1       CATALYTIC BASE.
FT   CONFLICT    105    105       N -> S (IN REF. 1).
SQ   SEQUENCE   114 AA;  12345 MW;  4BD525232B3F3069 CRC64;
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  Query Match           100.0%;  Score 26;  DB 1;  Length 114;
  Best Local Similarity  100.0%;  Pred. No. 13;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db      92 DRVYI 96


RESULT   5
MIF_MOUSE
ID   MIF_MOUSE      STANDARD;      PRT;   114 AA.
AC   P34884;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   MACROPHAGE MIGRATION INHIBITORY FACTOR (MIF) (PHENYLPYRUVATE
DE   TAUTOMERASE) (DELAYED EARLY RESPONSE PROTEIN 6) (DER6) (GLYCOSYLATION-
DE   INHIBITING FACTOR).
GN   MIF.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.
RC   TISSUE=Pituitary;
RX   MEDLINE=94019845; PubMed=8413654;
RA   Bernhagen J., Calandra T., Mitchell R.A., Martin S.B.,
RA   Tracey K.J., Voelter W., Manogue K.R., Cerami A., Bucala R.;
RT   "MIF is a pituitary-derived cytokine that potentiates lethal
RT   endotoxaemia.";
RL   Nature 365:756-759(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=92375060; PubMed=1508193;
RA   Lanahan A., Williams J.B., Sanders L.K., Nathans D.;
RT   "Growth factor-induced delayed early response genes.";
RL   Mol. Cell. Biol. 12:3919-3929(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94052102; PubMed=8234256;
RA   Mikayama T., Nakano T., Gomi H., Nakagawa Y., Liu Y.C., Iwamatsu A.,
RA   Weiser W.Y., Ishizaka K., Sato M., Ishii Y.;
RT   "Molecular cloning and functional expression of a cDNA encoding
RT   glycosylation-inhibiting factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:10056-10060(1993).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=95221891; PubMed=7706726;
RA   Mitchell R., Bacher M., Bernhagen J., Pushkarskaya T., Seldin M.F.,
RA   Bucala R.;
RT   "Cloning and characterization of the gene for mouse macrophage
RT   migration inhibitory factor (MIF).";
RL   J. Immunol. 154:3863-3870(1995).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=96047325; PubMed=7558021;
RA   Bozza M., Kolakowski L.F. Jr., Jenkins N.A., Gilbert D.J.,
RA   Copeland N.G., David J.R., Gerard C.;
RT   "Structural characterization and chromosomal location of the mouse
RT   macrophage migration inhibitory factor gene and pseudogenes.";
RL   Genomics 27:412-419(1995).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV;
RX   MEDLINE=96047324; PubMed=7558020;
RA   Kozak C.A., Adamson M.C., Buckler C.E., Segovia L., Paralkar V.,
RA   Wistow G.;
RT   "Genomic cloning of mouse MIF (macrophage inhibitory factor) and
```

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RT   genetic mapping of the human and mouse expressed gene and nine mouse
RT   pseudogenes.";
RL   Genomics 27:405-411(1995).
RN   [7]
RP   SEQUENCE OF 5-114 FROM N.A.
RC   TISSUE=Lens;
RX   MEDLINE=93165679; PubMed=7679497;
RA   Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;
RT   "A macrophage migration inhibitory factor is expressed in the
RT   differentiating cells of the eye lens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX   MEDLINE=99303983; PubMed=10360941;
RA   Taylor A.B., Johnson W.H. Jr., Czerwinski R.M., Li H.S., Hackert M.L.,
RA   Whitman C.P.;
RT   "Crystal structure of macrophage migration inhibitory factor
RT   complexed with (E)-2-fluoro-p-hydroxycinnamate at 1.8 A resolution:
RT   implications for enzymatic catalysis and inhibition.";
RL   Biochemistry 38:7444-7452(1999).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.00 ANGSTROMS).
RX   MEDLINE=20393856; PubMed=10933783;
RA   Stamps S.L., Taylor A.B., Wang S.C., Hackert M.L., Whitman C.P.;
RT   "Mechanism of the phenylpyruvate tautomerase activity of macrophage
RT   migration inhibitory factor: properties of the P1G, P1A, Y95F, and
RT   N97A mutants.";
RL   Biochemistry 39:9671-9678(2000).
CC   -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC       ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC       HOST DEFENSE. ALSO ACTS AS A PHENYLPYRUVATE TAUTOMERASE.
CC   -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z23048; CAA80583.1; -.
DR   EMBL; U19825; AAA91637.1; -.
DR   EMBL; L10613; AAA37693.1; -.
DR   EMBL; U20156; AAA91638.1; -.
DR   EMBL; L39357; AAA74321.1; -.
DR   EMBL; L07607; AAA37111.1; -.
DR   PIR; S34299; S34299.
DR   PIR; A44499; A44499.
DR   PDB; 1MFF; 11-AUG-00.
DR   PDB; 1MFI; 22-JUN-99.
DR   MGD; MGI:96982; Mif.
DR   InterPro; IPR001398; MIF.
DR   Pfam; PF01187; MIF; 1.
DR   PROSITE; PS01158; MIF; 1.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.
FT   INIT_MET      0      0
FT   ACT_SITE      1      1       CATALYTIC BASE.
SQ   SEQUENCE   114 AA;  12373 MW;  8FD2339CF0792F9E CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     92 DRVYI 96


RESULT   6
MIF_RAT
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ID   MIF_RAT        STANDARD;      PRT;   114 AA.
AC   P30904;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   MACROPHAGE MIGRATION INHIBITORY FACTOR (MIF) (PHENYLPYRUVATE
DE   TAUTOMERASE) (GLUTATHIONE-BINDING 13 KDA PROTEIN).
GN   MIF.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=95038523; PubMed=7951062;
RA   Sakai M., Nishihira J., Hibiya Y., Koyama Y., Nishi S.;
RT   "Glutathione binding rat liver 13k protein is the homologue of the
RT   macrophage migration inhibitory factor.";
RL   Biochem. Mol. Biol. Int. 33:439-446(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lens;
RA   Wen Y., Li G., Bekhor I.;
RL   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PVG/C;
RA   Sleeman M.A., Huckle J.W., Robinson M., Jahoda C.A.B.,
RA   Reynolds A.J., Whitehouse C.J.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1-25.
RX   MEDLINE=93063370; PubMed=1436109;
RA   Blocki F.A., Schlievert P.M., Wackett L.P.;
RT   "Rat liver protein linking chemical and immunological detoxification
RT   systems.";
RL   Nature 360:269-270(1992).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC   TISSUE=Liver;
RX   MEDLINE=96186248; PubMed=8605628;
RA   Suzuki M., Sugimoto H., Nakagawa A., Tanaka I., Nishihira J.,
RA   Sakai M.;
RT   "Crystal structure of the macrophage migration inhibitory factor from
RT   rat liver.";
RL   Nat. Struct. Biol. 3:259-266(1996).
CC   -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC       ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC       HOST DEFENSE. ALSO ACTS AS A PHENYLPYRUVATE TAUTOMERASE.
CC   -!- SUBUNIT: HOMOTRIMER.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF ORGANS
CC       INCLUDING BRAIN, SPLEEN, LIVER, MUSCLE AND KIDNEY.
CC   -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S73424; AAB32392.1; -.
DR   EMBL; U20999; AAA62644.1; -.
DR   EMBL; U62326; AAB04024.1; -.
DR   PDB; 1FIM; 11-JUL-96.
DR   InterPro; IPR001398; MIF.
DR   Pfam; PF01187; MIF; 1.
DR   PROSITE; PS01158; MIF; 1.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.
FT   INIT_MET      0      0
FT   ACT_SITE      1      1       CATALYTIC BASE (BY SIMILARITY).
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FT   CONFLICT     50     50       S -> R (IN REF. 2).
SQ   SEQUENCE   114 AA;  12346 MW;  9E33C39CF064329E CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db      92 DRVYI 96


RESULT   7
TBX6_HUMAN
ID   TBX6_HUMAN     STANDARD;      PRT;   436 AA.
AC   O95947;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   T-BOX TRANSCRIPTION FACTOR TBX6 (T-BOX PROTEIN 6).
GN   TBX6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99134303; PubMed=9933572;
RA   Papapetrou C., Putt W., Fox M., Edwards Y.H.;
RT   "The human TBX6 gene: cloning and assignment to chromosome 16p11.2.";
RL   Genomics 55:238-241(1999).
RN   [2]
RP   SEQUENCE OF 135-272 FROM N.A.
RC   TISSUE=Myeloid;
RX   MEDLINE=99107806; PubMed=9888994;
RA   Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,
RA   Amstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.;
RT   "Identification, mapping and phylogenomic analysis of four new human
RT   members of the T-box gene family: EOMES, TBX6, TBX18, and TBX19.";
RL   Genomics 55:10-20(1999).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF
CC       PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).
CC   -!- SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL BUD, POSTERIOR SPINAL
CC       TISSUE, INTERVERTEBRAL DISC AND TESTIS. ALSO EXPRESSED IN ADULT
CC       TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A
CC       SECOND PHASE IN SOME ADULT TISSUES.
CC   -!- SIMILARITY: CONTAINS A T-BOX DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ007989; CAA07812.1; -.
DR   EMBL; AJ010279; CAB37938.1; -.
DR   MIM; 602427; -.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   PRINTS; PR00938; BRACHYURY.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
KW   Transcription regulation; DNA-binding; Nuclear protein;
KW   Developmental protein.
FT   DNA_BIND    100    273       T-BOX.
FT   CONFLICT    207    207       H -> HV (IN REF. 2).
SQ   SEQUENCE   436 AA;  47017 MW;  438178BD31B966E9 CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 436;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db     170 DRVYI 174


RESULT   8
ANGT_SHEEP
ID   ANGT_SHEEP     STANDARD;      PRT;   476 AA.
AC   P20757;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   ANGIOTENSINOGEN PRECURSOR [CONTAINS: ANGIOTENSIN I; ANGIOTENSIN II].
GN   SERPINA8 OR AGT.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=95072318; PubMed=7765514;
RA   Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,
RA   Murakami K., Nakamura Y.;
RT   "Sequencing and expression of sheep angiotensinogen cDNA.";
RL   Biosci. Biotechnol. Biochem. 58:1884-1885(1994).
RN   [2]
RP   SEQUENCE OF 25-39.
RX   MEDLINE=86136099; PubMed=3081342;
RA   Fernley R.T., John M., Niall H.D., Coghlan J.P.;
RT   "Purification and characterization of ovine angiotensinogen.";
RL   Eur. J. Biochem. 154:597-601(1986).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D17520; BAA04470.1; -.
DR   PIR; A25406; A25406.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    476       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
FT   PEPTIDE      25     32       ANGIOTENSIN II.
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FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   476 AA;  51304 MW;  C8A517CD9FA029F7 CRC64;


  Query Match           100.0%;  Score 26;  DB 1;  Length 476;
  Best Local Similarity  100.0%;  Pred. No. 55;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     25 DRVYI 29


RESULT   9
ANGT_MOUSE
ID   ANGT_MOUSE     STANDARD;      PRT;   477 AA.
AC   P11859;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   ANGIOTENSINOGEN PRECURSOR [CONTAINS: ANGIOTENSIN I; ANGIOTENSIN II].
GN   SERPINA8 OR AGT.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88284703; PubMed=3397061;
RA   Clouston W.M., Evans B.A., Haralambidis J., Richards R.I.;
RT   "Molecular cloning of the mouse angiotensinogen gene.";
RL   Genomics 2:240-248(1988).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF045887; AAC01765.1; -.
DR   EMBL; AF045886; AAC01765.1; JOINED.
DR   EMBL; AF045885; AAC01765.1; JOINED.
DR   EMBL; AF045884; AAC01765.1; JOINED.
DR   PIR; A29978; A29978.
DR   MGD; MGI:87963; Agt.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; FALSE_NEG.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    477       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
FT   PEPTIDE      25     32       ANGIOTENSIN II.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    319    319       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    401    401       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   477 AA;  51990 MW;  A877F4029F338607 CRC64;


  Query Match           100.0%;  Score 26;  DB 1;  Length 477;
  Best Local Similarity  100.0%;  Pred. No. 55;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     25 DRVYI 29


RESULT  10
ANGT_RAT
ID   ANGT_RAT       STANDARD;      PRT;   477 AA.
AC   P01015;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   ANGIOTENSINOGEN PRECURSOR [CONTAINS: ANGIOTENSIN I; ANGIOTENSIN II].
GN   SERPINA8 OR AGT.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR;
RX   MEDLINE=83169849; PubMed=6572971;
RA   Ohkubo H., Kageyama R., Ujihara M., Hirose T., Inayama S.,
RA   Nakanishi S.;
RT   "Cloning and sequence analysis of cDNA for rat angiotensinogen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).
RN   [2]
RP   SEQUENCE OF 25-34.
RX   MEDLINE=73060322; PubMed=4344907;
RA   Nakayama T., Nakajima T., Sokabe H.;
RT   "Comparative studies on angiotensins. II. Structure of rat
RT   angiotensin and its identification by DNS-method.";
RL   Chem. Pharm. Bull. 20:1579-1581(1972).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L00094; AAA98779.1; -.
DR   EMBL; L00091; AAA98779.1; JOINED.
DR   EMBL; L00092; AAA98779.1; JOINED.
DR   EMBL; L00093; AAA98779.1; JOINED.
DR   PIR; A01251; ANRT.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; FALSE_NEG.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    477       ANGIOTENSINOGEN.
FT   PEPTIDE      25     34       ANGIOTENSIN I.
FT   PEPTIDE      25     32       ANGIOTENSIN II.
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    319    319       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   477 AA;  51981 MW;  689051A5788D693D CRC64;
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  Query Match           100.0%;  Score 26;  DB 1;  Length 477;
  Best Local Similarity  100.0%;  Pred. No. 55;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db      25 DRVYI 29


RESULT  11
ANGT_HUMAN
ID   ANGT_HUMAN     STANDARD;      PRT;   485 AA.
AC   P01019; Q16358; Q16359;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   ANGIOTENSINOGEN PRECURSOR [CONTAINS: ANGIOTENSIN I; ANGIOTENSIN II].
GN   SERPINA8 OR AGT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89170129; PubMed=2924688;
RA   Gaillard I., Clauser E., Corvol P.;
RT   "Structure of human angiotensinogen gene.";
RL   DNA 8:87-99(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85000455; PubMed=6089875;
RA   Kageyama R., Ohkubo H., Nakanishi S.;
RT   "Primary structure of human preangiotensinogen deduced from the
RT   cloned cDNA sequence.";
RL   Biochemistry 23:3603-3609(1984).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90237063; PubMed=1692023;
RA   Fukamizu A., Takahashi S., Seo M.S., Tada M., Tanimoto K., Uehara S.,
RA   Murakami K.;
RT   "Structure and expression of the human angiotensinogen gene.
RT   Identification of a unique and highly active promoter.";
RL   J. Biol. Chem. 265:7576-7582(1990).
RN   [4]
RP   SEQUENCE OF 1-338 FROM N.A.
RX   MEDLINE=87244745; PubMed=2885106;
RA   Kunapuli S.P., Kumar A.;
RT   "Molecular cloning of human angiotensinogen cDNA and evidence for the
RT   presence of its mRNA in rat heart.";
RL   Circ. Res. 60:786-790(1987).
RN   [5]
RP   SEQUENCE OF 34-43.
RX   MEDLINE=69014170; PubMed=4300938;
RA   Arakawa K., Minohara A., Yamada J., Nakamura M.;
RT   "Enzymatic degradation and electrophoresis of human angiotensin I.";
RL   Biochim. Biophys. Acta 168:106-112(1968).
RN   [6]
RP   STRUCTURE BY NMR OF ANGIOTENSIN II.
RX   MEDLINE=98151281; PubMed=9492317;
RA   Carpenter K.A., Wilkes B.C., Schiller P.W.;
RT   "The octapeptide angiotensin II adopts a well-defined structure in a
RT   phospholipid environment.";
RL   Eur. J. Biochem. 251:448-453(1998).
RN   [7]
RP   VARIANTS MET-207; THR-268 AND CYS-281.
RX   MEDLINE=93008239; PubMed=1394429;
RA   Jeunemaitre X., Soubrier F., Kotelevtsev Y.V., Lifton R.P.,
RA   Williams C.S., Charru A., Hunt S.C., Hopkins P.N., Williams R.R.,
RA   Lalouel J.-M., Corvol P.;
RT   "Molecular basis of human hypertension: role of angiotensinogen.";
RL   Cell 71:169-180(1992).
RN   [8]
RP   VARIANT THR-268.
RX   MEDLINE=93291876; PubMed=8513325;
RA   Ward K., Hata A., Jeunemaitre X., Helin C., Nelson L., Namikawa C.,
RA   Farrington P.F., Ogasawara M., Suzumori K., Tomoda S., Berrebi S.,
RA   Sasaki M., Corvol P., Lifton R.P., Lalouel J.-M.;
RT   "A molecular variant of angiotensinogen associated with
RT   preeclampsia.";
RL   Nat. Genet. 4:59-61(1993).
RN   [9]
RP   VARIANTS ILE-242; ARG-244 AND CYS-281.
RX   MEDLINE=95331754; PubMed=7607642;
RA   Hixson J.E., Powers P.K.;
RT   "Detection and characterization of new mutations in the human
RT   angiotensinogen gene (AGT).";
RL   Hum. Genet. 96:110-112(1995).
CC   -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC       CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC       CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC       PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC       PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC       BALANCE OF BODY FLUIDS.
CC   -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC   -!- DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO
CC       ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION
CC       (PIH) (PREECLAMPSIA).
CC   -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; K02215; AAA51731.1; -.
DR   EMBL; M24689; AAA51679.1; -.
DR   EMBL; M24686; AAA51679.1; JOINED.
DR   EMBL; M24687; AAA51679.1; JOINED.
DR   EMBL; M24688; AAA51679.1; JOINED.
DR   EMBL; X15324; CAA33385.1; -.
DR   EMBL; X15325; CAA33385.1; JOINED.
DR   EMBL; X15326; CAA33385.1; JOINED.
DR   EMBL; X15327; CAA33385.1; JOINED.
DR   EMBL; M69110; AAA52282.1; -.
DR   EMBL; S78529; AAD14287.1; -.
DR   EMBL; S78530; AAD14288.1; -.
DR   PIR; A01249; ANHU.
DR   PIR; A31362; A31362.
DR   PIR; A35203; A35203.
DR   SWISS-2DPAGE; P01019; HUMAN.
DR   MIM; 106150; -.
DR   InterPro; IPR000227; Angiotensngn.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   PRINTS; PR00654; ANGIOTENSNGN.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal;
KW   Disease mutation; Polymorphism.
FT   SIGNAL        1     33
FT   CHAIN        34    485       ANGIOTENSINOGEN.
FT   PEPTIDE      34     43       ANGIOTENSIN I.
FT   PEPTIDE      34     41       ANGIOTENSIN II.
FT   CARBOHYD     47     47       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    304    304       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    328    328       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     207    207       T -> M.
FT                                /FTId=VAR_007093.
FT   VARIANT     242    242       T -> I (IN HYPERTENSION).
FT                                /FTId=VAR_007094.
```

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FT   VARIANT     244    244       L -> R (IN HYPERTENSION).
FT                                /FTId=VAR_007095.
FT   VARIANT     268    268       M -> T (IN HYPERTENSION).
FT                                /FTId=VAR_007096.
FT   VARIANT     281    281       Y -> C (IN HYPERTENSION).
FT                                /FTId=VAR_007097.
FT   CONFLICT    333    333       Q -> E (IN REF. 1).
SQ   SEQUENCE   485 AA;  53154 MW;  5026C2DFB2DD236E CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 56;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db      34 DRVYI 38


RESULT  12
YB95_METJA
ID   YB95_METJA     STANDARD;      PRT;   518 AA.
AC   Q58595;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   PUTATIVE 2-ISOPROPYLMALATE/HOMOCITRATE SYNTHASE MJ1195 (EC 4.1.3.-).
GN   MJ1195.
OS   Methanococcus jannaschii.
OC   Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC   Methanococcus.
OX   NCBI_TaxID=2190;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX   MEDLINE=96337999; PubMed=8688087;
RA   Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA   Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA   Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA   Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA   Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA   Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA   Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA   Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT   "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT   jannaschii.";
RL   Science 273:1058-1073(1996).
CC   -!- SIMILARITY: BELONGS TO THE ALPHA-IPM SYNTHETASE / HOMOCITRATE
CC       SYNTHASE FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U67561; AAB99199.1; -.
DR   TIGR; MJ1195; -.
DR   InterPro; IPR002034; AIPM_homocit_synth.
DR   InterPro; IPR000891; HMGL-like.
DR   Pfam; PF00682; HMGL-like; 1.
DR   PROSITE; PS00815; AIPM_HOMOCIT_SYNTH_1; 1.
DR   PROSITE; PS00816; AIPM_HOMOCIT_SYNTH_2; 1.
KW   Hypothetical protein; Lyase; Complete proteome.
SQ   SEQUENCE   518 AA;  56620 MW;  604AB61B41E607A4 CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 518;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db      22 DRVYI 26


RESULT  13
TBX6_MOUSE
ID   TBX6_MOUSE     STANDARD;      PRT;   540 AA.
AC   P70327;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   T-BOX TRANSCRIPTION FACTOR TBX6 (T-BOX PROTEIN 6).
GN   TBX6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97032942; PubMed=8878690;
RA   Agulnik S.I., Garvey N., Hancock S., Ruvinsky I., Chapman D.L.,
RA   Agulnik I., Bollag R.J., Papaioannou V.E., Silver L.M.;
RT   "Evolution of mouse T-box genes by tandem duplication and cluster
RT   dispersion.";
RL   Genetics 144:249-254(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Gastrula;
RX   MEDLINE=97115702; PubMed=8954725;
RA   Chapman D.L., Agulnik I., Hancock S., Silver L.M., Papaioannou V.E.;
RT   "Tbx6, a mouse T-Box gene implicated in paraxial mesoderm formation at
RT   gastrulation.";
RL   Dev. Biol. 180:534-542(1996).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=98140705; PubMed=9490412;
RA   Chapman D.L., Papaioannou V.E.;
RT   "Three neural tubes in mouse embryos with mutations in the T-box gene
RT   Tbx6.";
RL   Nature 391:695-697(1998).
CC   -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC       DEVELOPMENTAL PROCESSES. REQUIRED FOR SPECIFICATION OF PARAXIAL
CC       MESODERM STRUCTURES DURING GASTRULATION. IN ITS ABSENCE CELLS
CC       DESTINED TO FORM POSTERIOR SOMITES DIFFERENTIATE ALONG A NEURONAL
CC       PATHWAY.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC   -!- DEVELOPMENTAL STAGE: TBX6 IS FIRST DETECTED IN THE GASTRULATION
CC       STAGE IN THE PRIMITIVE STREAK AND NEWLY RECRUITED PARAXIAL
CC       MESODERM. LATER IN DEVELOPMENT IT IS RESTRICTED TO PRESOMITIC,
CC       PARAXIAL MESODERM AND TO THE TAIL BUD, WHICH REPLACES THE STREAK
CC       AS THE SOURCE OF MESODERM.
CC   -!- SIMILARITY: CONTAINS A T-BOX DOMAIN.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U57331; AAC53110.1; -.
DR   HSSP; P24781; 1XBR.
DR   MGD; MGI:102539; Tbx6.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01283; TBOX_1; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
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KW   Transcription regulation; DNA-binding; Nuclear protein;
KW   Developmental protein.
FT   DOMAIN       61     64       POLY-ALA.
FT   DOMAIN       79     82       POLY-PRO.
FT   DNA_BIND    100    273       T-BOX.
SQ   SEQUENCE   540 AA;  58628 MW;  BC834CE2745E8E61 CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 62;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db    170 DRVYI 174


RESULT  14
HEMA_SEND5
ID   HEMA_SEND5     STANDARD;      PRT;   575 AA.
AC   P27562;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   HEMAGGLUTININ-NEURAMINIDASE (EC 3.2.1.18).
GN   HN.
OS   Sendai virus (strain Z / host mutants).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Paramyxovirus.
OX   NCBI_TaxID=11192;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MUTANT TS-F1, AND MUTANT F1-R;
RX   MEDLINE=90266486; PubMed=2161155;
RA   Middleton Y., Tashiro M., Thai T., Oh J., Seymour J., Pritzer E.,
RA   Klenk H.D., Rott R., Seto J.T.;
RT   "Nucleotide sequence analyses of the genes encoding the HN, M, NP, P,
RT   and L proteins of two host range mutants of Sendai virus.";
RL   Virology 176:656-657(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MUTANT F1-R / T-5 REVERTANT;
RX   MEDLINE=91335752; PubMed=1651590;
RA   Tashiro M., James I., Karri S., Wahn K., Tobita K., Klenk H.D.,
RA   Rott R., Seto J.T.;
RT   "Pneumotropic revertants derived from a pantropic mutant, F1-R, of
RT   Sendai virus.";
RL   Virology 184:227-234(1991).
CC   -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
CC       TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
CC       ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
CC       THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
CC       GLYCOPROTEINS.
CC   -!- CATALYTIC ACTIVITY: HYDROLYSIS OF ALPHA-(2->3)-, ALPHA-(2->6)-,
CC       ALPHA-(2->8)-GLYCOSIDIC LINKAGES OF TERMINAL SIALIC RESIDUES IN
CC       OLIGOSACCHARIDES, GLYCOPROTEINS, GLYCOLIPIDS, COLOMINIC ACID AND
CC       SYNTHETIC SUBSTRATES.
CC   -!- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
CC       N-TERMINAL HYDROPHOBIC SEQUENCE.
CC   -!- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
CC       NEURAMINIDASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M30202; AAB06282.1; -.
DR   EMBL; M30203; AAB06288.1; -.
DR   EMBL; M30204; AAB06200.1; -.
DR   EMBL; M69046; AAB06294.1; -.
DR   InterPro; IPR000665; Hem-neuramndse.
DR   Pfam; PF00423; HN; 1.
KW   Hydrolase; Hemagglutinin; Envelope protein; Glycoprotein;
KW   Transmembrane.
FT   DOMAIN       1     35       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    36     60       POTENTIAL.
FT   DOMAIN      61    575       EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD    77     77       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   499    499       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   511    511       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   575 AA;  63469 MW;  86EE95B73AD7EB2D CRC64;


  Query Match             100.0%;  Score 26;  DB 1;  Length 575;
  Best Local Similarity   100.0%;  Pred. No. 67;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db    419 DRVYI 423


RESULT  15
HEMA_SENDF
ID   HEMA_SENDF     STANDARD;      PRT;   575 AA.
AC   P19758;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   HEMAGGLUTININ-NEURAMINIDASE (EC 3.2.1.18).
GN   HN.
OS   Sendai virus (strain Fushimi).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Paramyxovirus.
OX   NCBI_TaxID=11195;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91057133; PubMed=2173829;
RA   Neubert W.J., Willenbrink W.;
RT   "Cloning and sequencing of the HN gene of Sendai virus (strain
RT   Fushimi).";
RL   Nucleic Acids Res. 18:6427-6427(1990).
CC   -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
CC       TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
CC       ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
CC       THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
CC       GLYCOPROTEINS.
CC   -!- CATALYTIC ACTIVITY: HYDROLYSIS OF ALPHA-(2->3)-, ALPHA-(2->6)-,
CC       ALPHA-(2->8)-GLYCOSIDIC LINKAGES OF TERMINAL SIALIC RESIDUES IN
CC       OLIGOSACCHARIDES, GLYCOPROTEINS, GLYCOLIPIDS, COLOMINIC ACID AND
CC       SYNTHETIC SUBSTRATES.
CC   -!- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
CC       N-TERMINAL HYDROPHOBIC SEQUENCE.
CC   -!- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
CC       NEURAMINIDASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X56131; CAA39596.1; -.
DR   PIR; S12135; S12135.
DR   PIR; S12462; S12462.
DR   InterPro; IPR000665; Hem-neuramndse.
DR   Pfam; PF00423; HN; 1.
KW   Hydrolase; Hemagglutinin; Envelope protein; Glycoprotein;
KW   Transmembrane.
FT   DOMAIN       1     35       CYTOPLASMIC (POTENTIAL).
```

```
FT   TRANSMEM     36     60       POTENTIAL.
FT   DOMAIN       61    575       EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD     77     77       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    499    499       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    511    511       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   575 AA;  63347 MW;  93FD0532F6147BF6 CRC64;


  Query Match           100.0%;  Score 26;  DB 1;  Length 575;
  Best Local Similarity  100.0%;  Pred. No. 67;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
             |||||
Db     419 DRVYI 423


Search completed: February 26, 2002, 08:18:04
Job time: 108 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 26, 2002, 08:15:41 ; Search time 22.88 Seconds
(without alignments)
31.965 Million cell updates/sec

Title: US-09-658-315-9
Perfect score: 26
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	100.0	14	5	Q10757	Q10757 theromyzon
2	26	100.0	72	2	Q9R540	Q9r540 clostridium
3	26	100.0	87	8	Q9G9H0	Q9g9h0 eretmocerus
4	26	100.0	167	2	Q9KG21	Q9kg21 bacillus ha
5	26	100.0	173	12	Q88184	Q88184 san miguel
6	26	100.0	178	1	Q9HIS3	Q9his3 thermoplasm
7	26	100.0	186	5	Q9W387	Q9w387 drosophila
8	26	100.0	195	1	O28741	O28741 archaeoglob
9	26	100.0	238	2	O66729	O66729 aquifex aeo
10	26	100.0	248	2	Q44326	Q44326 agrobacteri
11	26	100.0	291	3	Q9C445	Q9c445 penicillium
12	26	100.0	291	4	Q9HBV1	Q9hbv1 homo sapien
13	26	100.0	291	11	Q9ES81	Q9es81 mus musculu
14	26	100.0	295	4	Q9HA44	Q9ha44 homo sapien
15	26	100.0	312	10	O48726	O48726 arabidopsis
16	26	100.0	321	5	Q9GNL3	Q9gnl3 drosophila
17	26	100.0	340	12	Q9DVW3	Q9dvw3 plutella xy
18	26	100.0	369	13	Q9IAE7	Q9iae7 pantodon bu
19	26	100.0	377	13	Q9IAG5	Q9iag5 gymnarchus
20	26	100.0	408	10	Q9MA64	Q9ma64 arabidopsis
21	26	100.0	409	1	O27084	O27084 methanobact
22	26	100.0	461	11	Q9D2V0	Q9d2v0 mus musculu
23	26	100.0	485	6	Q9GLP7	Q9glp7 pan troglod
24	26	100.0	485	6	Q9GLP6	Q9glp6 gorilla gor
25	26	100.0	485	6	Q9GLN8	Q9gln8 pan troglod
26	26	100.0	486	6	Q9TSZ0	Q9tsz0 callithrix
27	26	100.0	509	10	Q9T0L4	Q9t0l4 arabidopsis
28	26	100.0	575	12	Q88413	Q88413 sendai viru
29	26	100.0	614	2	O87250	O87250 lactococcus
30	26	100.0	644	2	Q9KQX5	Q9kqx5 vibrio chol
31	26	100.0	661	2	Q9KCM3	Q9kcm3 bacillus ha
32	26	100.0	749	2	P73687	P73687 synechocyst
33	26	100.0	798	2	Q9EZL3	Q9ezl3 mycobacteri
34	26	100.0	838	3	O94653	O94653 schizosacch
35	26	100.0	1047	1	Q9HK17	Q9hk17 thermoplasm
36	26	100.0	1062	2	Q9K9V9	Q9k9v9 bacillus ha
37	26	100.0	1076	1	O28994	O28994 archaeoglob
38	26	100.0	1238	2	O25330	O25330 helicobacte
39	26	100.0	1280	5	Q9VZ55	Q9vz55 drosophila
40	26	100.0	1296	2	Q45894	Q45894 clostridium
41	26	100.0	1812	4	Q9ULL3	Q9ull3 homo sapien
42	26	100.0	2018	4	Q9NZM0	Q9nzm0 homo sapien
43	26	100.0	2048	4	Q9HBU3	Q9hbu3 homo sapien
44	26	100.0	2061	4	Q9NZM1	Q9nzm1 homo sapien
45	26	100.0	2433	12	O91464	O91464 aichi virus

ALIGNMENTS

RESULT 1
Q10757
ID Q10757 PRELIMINARY; PRT; 14 AA.
AC Q10757;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ANGIOTENSINOGEN (FRAGMENT).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RX MEDLINE=95365039; PubMed=7637887;
RA Laurent V., Bulet P., Salzet M.A.;
RT "A comparison of the leech Theromyzon tessulatum angiotensin I-like
RT molecule with forms of vertebrate angiotensinogens: a hormonal system
RT conserved in the course of evolution.";
RL Neurosci. Lett. 190:175-178(1995).
RN [2]
RP SEQUENCE OF 1-10.
RC TISSUE=BRAIN;
RX MEDLINE=96201949; PubMed=8612806;
RA Laurent V., Salzet M.;
RT "Metabolism of angiotensins by head membranes of the leech Theromyzon
RT tessulatum.";
RL FEBS Lett. 384:123-127(1996).
CC -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.
KW Glycoprotein; Serpin.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1763 MW; 335109D8EEEFBDD7 CRC64;

Query Match 100.0%; Score 26; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5
|||||
Db 1 DRVYI 5

```
RESULT   2
Q9R540
ID   Q9R540      PRELIMINARY;      PRT;    72 AA.
AC   Q9R540;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   NEUROTOXIN HEAVY CHAIN 18 KDA FRAGMENT (FRAGMENT).
OS   Clostridium botulinum.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1491;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94000342; PubMed=8397793;
RA   Gimenez J.A., DasGupta B.R.;
RT   "Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72,
RT   45, 42, and 18 kD fragments.";
RL   J. Protein Chem. 12:351-363(1993).
DR   HSSP; P10845; 3BTA.
SQ   SEQUENCE   72 AA;  8165 MW;  B7A959576A615E18 CRC64;


  Query Match             100.0%;  Score 26;  DB 2;  Length 72;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     31 DRVYI 35


RESULT   3
Q9G9H0
ID   Q9G9H0      PRELIMINARY;      PRT;    87 AA.
AC   Q9G9H0;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CYTOCHROME OXIDASE II (FRAGMENT).
OS   Eretmocerus mundus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC   Chalcidoidea; Aphelinidae; Eretmocerus.
OX   NCBI_TaxID=77302;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   De Barro P.J., Driver F., Naumann I.D., Clarke G.M., Curran J.;
RT   "Descriptions of three species of Eretmocerus Haldeman (Hymenoptera:
RT   Aphelinidae) parasitising Bemisia tabaci (Gennadius) (Hemiptera:
RT   Aleyrodidae) and Trialeurodes vaporariorum (Westwood) (Hemiptera:
RT   Aleyrodidae) in Australia based on morphological and molecular data.";
RL   Aust. J. Entomol. 0:0-0(2000).
DR   EMBL; AF275275; AAG25079.1; -.
DR   InterPro; IPR001505; COX2.
DR   InterPro; IPR002429; Cyt_c_ox_2.
DR   Pfam; PF00116; COX2; 1.
DR   PRINTS; PR01166; CYCOXIDASEII.
DR   ProDom; PD000131; COX2; 1.
KW   Mitochondrion.
FT   NON_TER       1      1
FT   NON_TER      87     87
SQ   SEQUENCE   87 AA;  10387 MW;  43E205FB2E1C6FEC CRC64;


  Query Match             100.0%;  Score 26;  DB 8;  Length 87;
  Best Local Similarity   100.0%;  Pred. No. 79;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     81 DRVYI 85


RESULT   4
Q9KG21
ID   Q9KG21      PRELIMINARY;      PRT;   167 AA.
AC   Q9KG21;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   BH0294 PROTEIN.
GN   BH0294.
OS   Bacillus halodurans.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Bacillus.
OX   NCBI_TaxID=86665;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C-125 / JCM 9153;
RX   MEDLINE=20512582; PubMed=11058132;
RA   Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA   Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA   Horikoshi K.;
RT   "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT   halodurans and genomic sequence comparison with Bacillus subtilis.";
RL   Nucleic Acids Res. 28:4317-4331(2000).
DR   EMBL; AP001508; BAB04013.1; -.
KW   Complete proteome.
SQ   SEQUENCE   167 AA;  19535 MW;  0C33F04D1A2E834D CRC64;


  Query Match             100.0%;  Score 26;  DB 2;  Length 167;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     61 DRVYI 65


RESULT   5
Q88184
ID   Q88184      PRELIMINARY;      PRT;   173 AA.
AC   Q88184;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   RNA-DEPENDENT RNA POLYMERASE (FRAGMENT).
OS   San Miguel sea lion virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC   Vesivirus.
OX   NCBI_TaxID=11982;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SEROTYPE 5;
RX   MEDLINE=95287505; PubMed=7769708;
RA   Neill J.D., Meyer R.F., Seal B.S.;
RT   "Genetic relatedness of the caliciviruses: San Miguel sea lion and
RT   vesicular exanthema of swine viruses constitute a single genotype
RT   within the Caliciviridae.";
RL   J. Virol. 69:4484-4488(1995).
DR   EMBL; U18731; AAA82219.1; -.
DR   InterPro; IPR001643; Calici_coat.
DR   PRINTS; PR00918; CALICVIRUSNS.
KW   RNA-directed RNA polymerase.
FT   NON_TER       1      1
FT   NON_TER     173    173
SQ   SEQUENCE   173 AA;  19532 MW;  1830C8461CC21F7F CRC64;


  Query Match             100.0%;  Score 26;  DB 12;  Length 173;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 DRVYI 5
          |||||
Db     50 DRVYI 54


RESULT   6
Q9HIS3
ID   Q9HIS3      PRELIMINARY;      PRT;   178 AA.
AC   Q9HIS3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PROBABLE 50S RIBOSOMAL PROTEIN L6.
GN   TA1255.
OS   Thermoplasma acidophilum.
OC   Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
OC   Thermoplasma.
OX   NCBI_TaxID=2303;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DSM 1728;
RX   MEDLINE=20479972; PubMed=11029001;
RA   Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA   Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT   "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT   acidophilum.";
RL   Nature 407:508-513(2000).
DR   EMBL; AL445067; CAC12379.1; -.
DR   InterPro; IPR000702; Ribosomal_L6.
DR   Pfam; PF00347; Ribosomal_L6; 1.
DR   ProDom; PD002236; Ribosomal_L6; 1.
KW   Ribosomal protein; Complete proteome.
SQ   SEQUENCE   178 AA;  19641 MW;  33B1312C268886A5 CRC64;

  Query Match             100.0%;  Score 26;  DB 1;  Length 178;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db    134 DRVYI 138


RESULT   7
Q9W387
ID   Q9W387      PRELIMINARY;      PRT;   186 AA.
AC   Q9W387;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CG12664 PROTEIN.
GN   LD14 OR CG12664.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003446; AAF46447.1; -.
DR   FlyBase; FBgn0030090; ld14.
SQ   SEQUENCE   186 AA;  20461 MW;  D2B4ED097ACA6420 CRC64;

  Query Match             100.0%;  Score 26;  DB 5;  Length 186;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db    110 DRVYI 114


RESULT   8
O28741
ID   O28741      PRELIMINARY;      PRT;   195 AA.
AC   O28741;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   CONSERVED HYPOTHETICAL PROTEIN.
GN   AF1531.
OS   Archaeoglobus fulgidus.
OC   Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC   Archaeoglobus.
OX   NCBI_TaxID=2234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX   MEDLINE=98049343; PubMed=9389475;
RA   Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA   Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA   Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA   Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA   Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA   Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA   Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA   Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA   Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA   Venter J.C.;
RT   "The complete genome sequence of the hyperthermophilic, sulphate-
RT   reducing archaeon Archaeoglobus fulgidus.";
RL   Nature 390:364-370(1997).
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DR   EMBL; AE000997; AAB89717.1; -.
DR   TIGR; AF1531; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   195 AA;  23194 MW;  C244F95420565E2C CRC64;


  Query Match           100.0%;  Score 26;  DB 1;  Length 195;
  Best Local Similarity  100.0%;  Pred. No. 2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     68 DRVYI 72


RESULT   9
O66729
ID   O66729      PRELIMINARY;      PRT;   238 AA.
AC   O66729;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ABC TRANSPORTER.
GN   ABCT7 OR AQ_413.
OS   Aquifex aeolicus.
OC   Bacteria; Aquificales; Aquificaceae; Aquifex.
OX   NCBI_TaxID=63363;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VF5;
RX   MEDLINE=98196666; PubMed=9537320;
RA   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA   Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA   Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT   "The complete genome of the hyperthermophilic bacterium Aquifex
RT   aeolicus.";
RL   Nature 392:353-358(1998).
CC   -!- SIMILARITY: TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC
CC       TRANSPORTERS).
DR   EMBL; AE000689; AAC06695.1; -.
DR   InterPro; IPR003593; AAA.
DR   InterPro; IPR003439; ABC_transportr.
DR   InterPro; IPR001687; ATP_GTP_A.
DR   Pfam; PF00005; ABC_tran; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW   ATP-binding; Complete proteome; Transport.
SQ   SEQUENCE   238 AA;  26457 MW;  032A46CD90CEA8E5 CRC64;


  Query Match           100.0%;  Score 26;  DB 2;  Length 238;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db    202 DRVYI 206


RESULT  10
Q44326
ID   Q44326      PRELIMINARY;      PRT;   248 AA.
AC   Q44326;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MOCC PROTEIN.
GN   MOCC.
OS   Agrobacterium radiobacter.
OG   Plasmid pTi15955.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=358;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=15955;
RX   MEDLINE=96236046; PubMed=8655509;
RA   Kim K.S., Farrand S.K.;
RT   "Ti plasmid-encoded genes responsible for catabolism of the crown gall
RT   opine mannopine by Agrobacterium tumefaciens are homologs of the T-
RT   region genes responsible for synthesis of this opine by the plant
RT   tumor.";
RL   J. Bacteriol. 178:3275-3284(1996).
CC   -!- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR)
CC       FAMILY.
DR   EMBL; AF242881; AAB07783.1; -.
DR   InterPro; IPR002198; ADH_short.
DR   Pfam; PF00106; adh_short; 1.
DR   PRINTS; PR00080; SDRFAMILY.
KW   Oxidoreductase; Plasmid.
SQ   SEQUENCE   248 AA;  26810 MW;  10B69239CDEBB68D CRC64;


  Query Match           100.0%;  Score 26;  DB 2;  Length 248;
  Best Local Similarity  100.0%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db    221 DRVYI 225


RESULT  11
Q9C445
ID   Q9C445      PRELIMINARY;      PRT;   291 AA.
AC   Q9C445;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PAXU.
GN   PAXU.
OS   Penicillium paxilli.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX   NCBI_TaxID=70109;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=11169115;
RA   Young C., McMillan L., Telfer E., Scott B.;
RT   "Molecular cloning and genetic analysis of an indole-diterpene gene
RT   cluster from Penicillium paxilli.";
RL   Mol. Microbiol. 39:754-764(2001).
DR   EMBL; AF279808; AAK11532.1; -.
SQ   SEQUENCE   291 AA;  32954 MW;  CFC35136FD40763E CRC64;


  Query Match           100.0%;  Score 26;  DB 3;  Length 291;
  Best Local Similarity  100.0%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DRVYI 5
          |||||
Db     16 DRVYI 20


RESULT  12
Q9HBV1
ID   Q9HBV1      PRELIMINARY;      PRT;   291 AA.
AC   Q9HBV1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   POPEYE PROTEIN 3.
GN   POP3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20341060; PubMed=10882522;
RA   Andree B., Hillemann T., Kessler-Icekson G., Schmitt-John T.,
RA   Jockusch H., Arnold H.H., Brand T.;
RT   "Isolation and characterization of the novel popeye gene family
RT   expressed in skeletal muscle and heart.";
RL   Dev. Biol. 223:371-382(2000).
DR   EMBL; AF204171; AAG23404.1; -.
SQ   SEQUENCE   291 AA;  33810 MW;  49B6EF5DBC02DDC2 CRC64;


  Query Match             100.0%;  Score 26;  DB 4;  Length 291;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db     248 DRVYI 252


RESULT  13
Q9ES81
ID   Q9ES81      PRELIMINARY;      PRT;   291 AA.
AC   Q9ES81;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   POPEYE PROTEIN 3.
GN   POP3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20341060; PubMed=10882522;
RA   Andree B., Hillemann T., Kessler-Icekson G., Schmitt-John T.,
RA   Jockusch H., Arnold H.H., Brand T.;
RT   "Isolation and characterization of the novel popeye gene family
RT   expressed in skeletal muscle and heart.";
RL   Dev. Biol. 223:371-382(2000).
DR   EMBL; AF204176; AAG23409.1; -.
DR   MGD; MGI:1930153; Pop3.
SQ   SEQUENCE   291 AA;  33612 MW;  8AC6BFE107AEEE12 CRC64;


  Query Match             100.0%;  Score 26;  DB 11;  Length 291;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db     248 DRVYI 252


RESULT  14
Q9HA44
ID   Q9HA44      PRELIMINARY;      PRT;   295 AA.
AC   Q9HA44;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CDNA FLJ12268 FIS, CLONE MAMMA1001627, HIGHLY SIMILAR TO HOMO SAPIENS
DE   TRANSCRIPTION FACTOR TBX6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY GLAND;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK022330; BAB14014.1; -.
DR   InterPro; IPR001699; T-box.
DR   Pfam; PF00907; T-box; 1.
DR   PRINTS; PR00937; TBOX.
DR   SMART; SM00425; TBOX; 1.
DR   PROSITE; PS01264; TBOX_2; 1.
DR   PROSITE; PS50252; TBOX_3; 1.
SQ   SEQUENCE   295 AA;  33197 MW;  F2BD3E53E0ED21E0 CRC64;


  Query Match             100.0%;  Score 26;  DB 4;  Length 295;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DRVYI 5
           |||||
Db     170 DRVYI 174


RESULT  15
O48726
ID   O48726      PRELIMINARY;      PRT;   312 AA.
AC   O48726;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   T9J22.26 PROTEIN.
GN   T9J22.26.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA   Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
RA   Somerville C.R., Venter J.C.;
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC002505; AAC14506.1; -.
SQ   SEQUENCE   312 AA;  34764 MW;  229F3B94EF849310 CRC64;


  Query Match             100.0%;  Score 26;  DB 10;  Length 312;
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Qy       1 DRVYI 5
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Db      81 DRVYI 85


Search completed: February 26, 2002, 08:17:48
Job time: 127 sec
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